GenCore version 5.1.4_p5_4578

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 11:25:23 ; Search time 7565 Seconds
(without alignments)
262.559 Million cell updates/sec

Title: US-10-070-464-1
Perfect score: 4700
Sequence: 1 MAAAMETEQLGVEIFETADC.....HLLHYLQENLGSRIAALKVI 882

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=75 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070464_@CGN_1_1_396_@runat_13052003_140014_29617 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4700	100.0	2671	24	ABK83322	cDNA encoding huma
2	4700	100.0	3106	24	ABK12892	Human protease PRT
3	4700	100.0	3120	22	AAC85694	Nucleotide sequenc
4	4700	100.0	3120	24	AAD38956	Human dipeptidyl p
5	4700	100.0	3143	24	AAH99934	cDNA encoding 2195
6	4695	99.9	2643	24	AAH99935	Coding sequence of
7	4680	99.6	4829	24	ABK83327	cDNA encoding huma
8	4385.5	93.3	4685	24	ABK83332	cDNA encoding huma
9	4385	93.3	4676	24	ABK83331	cDNA encoding huma
10	4118	87.6	2842	24	ABN59774	Novel human coding
11	4092.5	87.1	4523	24	ABK83325	cDNA encoding huma
12	3970.5	84.5	2510	24	AAD23843	Human protease PRT
13	3771	80.2	2668	24	ABN59775	Novel human coding
14	3661.5	77.9	4309	24	ABK83328	cDNA encoding huma
15	3364.5	71.6	2161	22	AAH15009	Human cDNA sequenc
16	2870	61.1	2617	24	ABK83323	cDNA encoding huma
17	2870	61.1	4219	24	ABK83335	cDNA encoding huma
18	2870	61.1	4302	24	ABK83333	cDNA encoding huma
19	2863	60.9	3024	24	AAD38954	Human dipeptidyl p
20	2835	60.3	2495	24	AAD38957	Human dipeptidyl p
21	2833	60.3	3287	24	AAD38955	Alternative versio
22	2820.5	60.0	4180	24	ABK83339	cDNA encoding huma
23	2820.5	60.0	4263	24	ABK83338	cDNA encoding huma
24	2763	58.8	2751	24	AAD38311	Murine dipeptidyl
25	2649	56.4	4076	24	ABK83337	cDNA encoding huma
26	2649	56.4	4159	24	ABK83336	cDNA encoding huma
27	2638	56.1	2801	22	AAI57896	Human polynucleoti
28	2599.5	55.3	4037	24	ABK83341	cDNA encoding huma
29	2599.5	55.3	4120	24	ABK83340	cDNA encoding huma
30	2476.5	52.7	3262	22	AAI57880	Human polynucleoti
31	2422	51.5	1669	22	AAC85696	Nucleotide sequenc
32	2226.5	47.4	2982	22	AAI59666	Human polynucleoti
33	1914.5	40.7	2461	21	AAC75835	Human ORFX ORF1390
34	1878.5	40.0	2952	24	ABK69090	DNA encoding human
35	1874.5	39.9	3047	24	ABK69113	DNA encoding human
36	1836.5	39.1	1083	22	AAC85697	Nucleotide sequenc
37	1645.5	35.0	1197	22	AAC85695	Nucleotide sequenc
38	1644.5	35.0	2027	21	AAC77137	Human ORFX ORF2692
39	1599.5	34.0	3713	23	ABL10425	Drosophila melanog
40	1599.5	34.0	3783	23	ABL06641	Drosophila melanog
41	1400	29.8	2079	21	AAA37672	Human peptidase, H
42	1391	29.6	2411	24	ABK83334	cDNA encoding huma
43	1370.5	29.2	2034	22	AAI59682	Human polynucleoti
44	1360	28.9	6225	23	ABL10424	Drosophila melanog
45	1360	28.9	6228	23	ABL06640	Drosophila melanog
46	1351	28.7	1837	24	ABK69114	DNA encoding human
47	1278	27.2	1356	24	ABK83326	cDNA encoding huma
48	1063	22.6	631	22	AAH07860	Human cDNA clone (
49	1026.5	21.8	832	24	ABK83330	cDNA encoding huma
50	929	19.8	873	22	AAF81719	Human protease and
51	927	19.7	925	24	ABL90148	Human polynucleoti
52	755.5	16.1	823	24	ABK30401	Human G-protein-co
53	736	15.7	1048	22	AAS41004	cDNA encoding nove
54	668	14.2	662	22	AAK92083	Human cDNA 5'-end
55	668	14.2	662	22	AAK93366	Human cDNA clone r
56	668	14.2	1748	22	AAK94819	Human full-length
57	665.5	14.2	561	22	AAL00876	Human reproductive
58	597.5	12.7	2313	20	AAX00013	Aspergillus oryzae
59	597.5	12.7	5496	20	AAX07327	Aspergillus oryzae
60	572	12.2	2199	21	AAA75238	Nucleotide sequenc
61	529	11.3	3407	24	ABK92227	Prostate cancer-as
62	526	11.2	2924	15	AAQ63261	CD26 cDNA clone.
63	525	11.2	2924	14	AAQ46089	Sequence of human
64	524	11.1	4835	24	ABK63663	Rat sequence diffe
c 65	475.5	10.1	587	22	AAH12830	Human cDNA clone (
66	466.5	9.9	2505	23	ABL29869	Drosophila melanog
67	464	9.9	620	24	ABK83329	cDNA encoding huma

68	461	9.8	2388	24	ABA05888	Human aminopeptida
69	461	9.8	2583	24	ABK83324	cDNA encoding huma
70	461	9.8	3238	24	ABA05887	Human aminopeptida
71	461	9.8	4541	24	ABK83342	cDNA encoding huma
72	456.5	9.7	2967	23	ABL17649	Drosophila melanog
73	455	9.7	3224	24	AAS94862	Human DNA sequence
74	454	9.7	2814	24	ABL62162	Colon adenocarcino
75	454	9.7	2814	24	ABL63097	Breast cancer rela

ALIGNMENTS

RESULT 1
ABK83322
ID ABK83322 standard; cDNA; 2671 BP.
XX
AC ABK83322;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPPIV related serine protease DPRP-1.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61591.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Claim 1; Page 53-54; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 2671 BP; 805 A; 524 C; 594 G; 748 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 2671

Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-070-464-1 (1-882) x ABK83322 (1-2671)

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Db      8 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 67

Qy     21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
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Db     68 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 127

Qy     41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
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Db    128 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 187

Qy     61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
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Db    188 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 247

Qy     81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
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Db    248 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 307

Qy    101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
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Db    308 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 367

Qy    121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 427

Qy    141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
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Qy    161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 547

Qy    181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
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Qy    201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
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Qy    221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
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Qy    241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
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Qy    261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
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Qy    301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
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Qy    321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
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Db    968 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1027

Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360

Db   1028 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1087

Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380

Db   1088 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1147

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400

Db   1148 CGCTCCCAGACTCGCCTGCAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1207

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420

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Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440

Db   1268 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1327

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460

Db   1328 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1387

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480

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Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500

Db   1448 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1507

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520

Db   1508 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1567

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540

Db   1568 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1627

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560

Db   1628 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1687

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580

Db   1688 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1747

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600

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Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620

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Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640

Db   1868 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 1927

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660

Db   1928 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTG 1987

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680

Db   1988 GTGAATAATCGATTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2047

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700

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Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

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Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740

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Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760

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Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780

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Qy    801 LysProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820

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Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840

Db   2468 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2527

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860

Db   2528 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2587

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880

Db   2588 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2647

Qy    881 ValIle 882

Db   2648 GTGATA 2653
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RESULT 2
ABK12892
ID ABK12892 standard; cDNA; 3106 BP.
XX
AC ABK12892;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PRTS-9 cDNA sequence.
XX
KW Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
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XX
PN WO200198468-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US19178.
XX
PR 16-JUN-2000; 2000US-212336P.

PR 22-JUN-2000; 2000US-213955P.
PR 29-JUN-2000; 2000US-215396P.
PR 07-JUL-2000; 2000US-216821P.
PR 14-JUL-2000; 2000US-218946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM;
PI Delegeane AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA;
PI Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT;
PI Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;
PI Kallick DA;
XX
DR WPI; 2002-090437/12.
DR P-PSDB; AAU74749.
XX
PT Twenty one human proteases (referred to as PRTS-1 to PRTS-21), useful
PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
PT proliferative (e.g. cancer)disorders -
XX
PS Claim 5; Page 166-167; 177pp; English.
XX
CC The present invention relates to twenty one new human proteases,
CC referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
CC myocardial infarction, autoimmune/inflammatory e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
CC endometriosis disorders. Numerous other examples of each disorder are
CC given in the specification. The present nucleic acid sequence encodes
CC the human protease PRTS-9 protein of the invention.
XX
SQ Sequence 3106 BP; 928 A; 633 C; 704 G; 841 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3106
Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-070-464-1 (1-882) x ABK12892 (1-3106)

```
Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys  20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     203 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 262

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     263 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 322

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     323 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 382

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     383 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 442

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     443 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 502

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     503 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 562

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     563 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 622

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     623 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 682

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     683 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 742

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     743 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 802

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     803 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 862

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     863 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 922

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     923 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 982

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     983 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1042

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
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Db    1043 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1102

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1103 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1162

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1163 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1222

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1223 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1282

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1283 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1342

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
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Db    1343 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1402

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
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Db    1403 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1462

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1463 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1522

Qy     441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1523 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1582

Qy     461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1583 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1642

Qy     481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
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Db   1643 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1702

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
Db   1703 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1762

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
Db   1763 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1822

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
Db   1823 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1882

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
Db   1883 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1942

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
Db   1943 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2002

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
Db   2003 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2062

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
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Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
Db   2123 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTG 2182

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
Db   2183 GTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2242

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
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Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
Db   2303 GCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2362

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740
Db   2363 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2422

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
Db   2423 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2482

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
Db   2483 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2542

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
Db   2543 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2602

Qy    801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
Db   2603 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2662

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
Db   2663 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2722

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
Db   2723 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2782

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
Db   2783 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2842

Qy    881 ValIle 882
Db   2843 GTGATA 2848
```

RESULT 3
AAC85694
ID AAC85694 standard; cDNA; 3120 BP.
XX
AC AAC85694;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of human DPP8.
XX
KW Human; dipeptidyl aminopeptidase; DPP8; prolyl oligopeptidase;
KW dipeptidyl peptidase; DPPIV; T cell; cleavage; diarrhoea;
KW growth hormone deficiency; glucose level; mucosal regeneration;
KW non-insulin dependent diabetes mellitus;glucose intolerance;
KW immunosuppression; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..2862
FT /*tag= a
FT /product= "Human DPP8"
XX
PN WO200119866-A1.
XX
PD 22-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-AU01085.
XX
PR 10-SEP-1999; 99AU-0002762.
PR 18-FEB-2000; 2000AU-0005709.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorell MD;
XX
DR WPI; 2001-281520/29.
DR P-PSDB; AAB47187.
XX
PT New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
PT substrates, identifying inhibitors of DPP8 catalytic activity which
PT have therapeutic uses, and for detecting activated T cells
XX
PS Claim 16; Fig 2; 78pp; English.
XX
CC This sequence encodes human dipeptidyl aminopeptidase (DPP8). DPP8
CC has substrate specificity for H-Ala-Pro-pNA, H-Gly-Pro-pNA and
CC H-Arg-Pro-pNA. Therefore, it is a prolyl oligopeptidase and a
CC dipeptidyl peptidase, because it is capable of hydrolysing the
CC peptide bond C-terminal to Pro in each of these compounds. DPP8
CC is homologous with human DPPIV. DPP8 is useful for cleaving a
CC substrate, and for detecting an activated T cell which involves
CC measuring the level of DPP8 gene expression in a T cell. The level
CC of DPP8 expression is detected by detecting the amount of DPP8 RNA
CC in the cell. It is also useful for identifying a molecule capable
CC of inhibiting the cleavage of the substrate by DPP8. Molecules
CC identified as inhibiting DPP8 catalytic activity may be useful for
CC treating diarrhoea, growth hormone deficiency, lowering glucose levels
CC in non-insulin dependent diabetes mellitus and other disorders
CC involving glucose intolerance, enhancing mucosal regeneration and
CC as immunosuppressants.
XX
SQ Sequence 3120 BP; 936 A; 637 C; 706 G; 841 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3120
Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-070-464-1 (1-882) x AAC85694 (1-3120)

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Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys  20
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Db     214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet  60
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Db     334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer  80
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Db     394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
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Db     454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
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Db     514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
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Db     574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
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Db     634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
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Db     694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 GATCCAAAATTATGCCCCGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
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Db     934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
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Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
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Db    1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
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Db    1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
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Db    1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
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Db    1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
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Db    1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
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Db    1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
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Db    1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy     441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy     461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
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Db    1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy     481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
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Qy     501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy     521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy     541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy     561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953

Qy     581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy     601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2014 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2073

Qy     621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2074 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2133

Qy     641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2134 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTG 2193

Qy     661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2194 GTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2253
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Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2254 TATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAGGC 2313

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2314 GCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2373

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2374 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2433

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
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Db   2434 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2493

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2494 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2553

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2554 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2613

Qy    801 LysProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2614 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2673

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2674 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2733

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2734 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2793

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2794 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2853

Qy    881 ValIle 882
          ||||||
Db   2854 GTGATA 2859

RESULT 4
AAD38956
ID   AAD38956 standard; cDNA; 3120 BP.
XX
AC   AAD38956;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human dipeptidyl peptidase 8 (DPP8) cDNA.
XX
KW   Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW   autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW   graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             214..2862
FT                   /*tag= a
FT                   /product= "Human DPP8 protein"
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
DR   WPI; 2002-454646/48.
DR   P-PSDB; AAE24170.
XX
PT   New dipeptidyl peptidase (DPP) peptides, useful for screening
PT   inhibitors of DPP catalytic activity, which may be employed to treat
PT   e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT   rejection and HIV infection -
XX
PS   Example; Fig 1; 91pp; English.
XX
CC   The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC   polynucleotides encoding such proteins. The DPP peptides are useful for
CC   screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC   for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC   rejection and HIV (human immuno deficiency virus) infection. The present
CC   sequence is human DPP8 cDNA.
XX
SQ   Sequence 3120 BP; 936 A; 637 C; 706 G; 841 T; 0 other;

Alignment Scores:
Pred. No.:                0          Length:          3120
Score:                    4700.00    Matches:         882
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0
DB:                       24         Gaps:            0

US-10-070-464-1 (1-882) x AAD38956 (1-3120)

Qy      1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy     21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy     41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy     61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy     81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy    101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy    121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy    141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy    161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy    181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy    201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 GATCCAAAATTATGCCCCGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy    221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy    241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy    261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy    281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy    301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy    321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293

Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
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Db   1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1713

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2014 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2073

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2074 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2133

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
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Db   2134 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTG 2193

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2194 GTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2253

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
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Db   2254 TATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAGGC 2313

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
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Db   2314 GCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2373

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2374 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2433

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
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Db   2434 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2493

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2494 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2553

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2554 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2613

Qy    801 LysProProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2614 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2673

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2674 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2733

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2734 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2793

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2794 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2853

Qy    881 ValIle 882
          ||||||
Db   2854 GTGATA 2859

RESULT 5
AAH99934
ID   AAH99934 standard; cDNA; 3143 BP.
XX
```

```
AC   AAH99934;
XX
DT   12-APR-2002  (first entry)
XX
DE   cDNA encoding 21953 human prolyl oligopeptidase.
XX
KW   21953 prolyl oligopeptidase; human; proline; endopeptidase;
KW   cancer; cardiovascular disease; autoimmune disease; atopic allergy;
KW   neuronal disorder; vascular disorder; prostate disorder; cytostatic;
KW   antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
KW   diabetes mellitus; arthritis; multiple sclerosis; asthma;
KW   Grave's disease; neuronal disorder; demyelinating disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             229..2877
FT                   /*tag= a
FT                   /product= "21953 prolyl oligopeptidase"
FT                   /note= "This region is specifically claimed in
FT                   claim 2"
XX
PN   WO200179473-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US40483.
XX
PR   18-APR-2000; 2000US-197508P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers RA,  Williamson M;
XX
DR   WPI; 2002-034353/04.
DR   P-PSDB; AAG78415.
XX
PT   New polypeptides 21953, member of human prolyl oligopeptidase family,
PT   useful as diagnostic targets and therapeutic agents for controlling
PT   cancer, lymphoma and leukemia  -
XX
PS   Claim 7; Page 100-102; 121pp; English.
XX
CC   This invention relates to an isolated 21953 human prolyl
CC   oligopeptidase. Which is cytostatic, antidiabetic, antiarthritic,
CC   neuroprotective, antithyroid, dermatological, antipsoriatic,
CC   antiasthmatic, ophthalmological, antiinflammatory, nootropic,
CC   antiparkinsonian, anticonvulsant, gynaecological, vasotropic,
CC   antianginal, cardiant, antiatherosclerotic, anorectic and
CC   metabolic in its action. Uses include gene therapy, expression or
CC   activity of 21953 protein modulator, it is useful for identifying a
CC   compound which binds to it and can be used in preventing, treating
CC   or detecting a cellular proliferative or differentiative disorder.
CC   The 21953 molecules can act as novel diagnostic targets and therapeutic
CC   agents for controlling disorders associated with the aberrant activity
CC   or degradation of peptide hormones e.g., disorders associated with cell
CC   differentiation and proliferation such as cancer, immune function,
CC   reproductive, neurological and cardiovascular function. The 21953
CC   molecules are thus useful for treating and preventing cellular
CC   proliferative and differentiative disorders, haematopoietic neoplastic
CC   disorders, immune disorders such as autoimmune diseases, diabetes
CC   mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
CC   neuronal disorders, demyelinating diseases, vascular disorders and
CC   metabolism or pain disorders. This sequence represents the cDNA
CC   encoding sequence of 21953 human prolyl oligopeptidase.
XX
SQ   Sequence 3143 BP; 943 A; 644 C; 712 G; 844 T; 0 other;

Alignment Scores:
Pred. No.:                0          Length:          3143
Score:                    4700.00    Matches:         882
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0

Query Match:              100.00%    Indels:          0
DB:                       24         Gaps:            0

US-10-070-464-1 (1-882) x AAH99934 (1-3143)

Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
Db     229 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 288

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
Db     289 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 348

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
Db     349 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 408

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
Db     409 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 468

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
Db     469 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 528

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
Db     529 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 588

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
Db     589 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 648

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
Db     649 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 708

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
Db     709 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 768

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
Db     769 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 828

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
Db     829 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 888

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
Db     889 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 948

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
Db     949 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 1008

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
Db    1009 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1068

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
Db    1069 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1128

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
Db    1129 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1188

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
Db    1189 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1248
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Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1308

Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1368

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CGCTCCCAGACTCGCCTGCAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1428

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1488

Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1548

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1608

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1668

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1728

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1788

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1848

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1908

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1968

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2028

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2088

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2148

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTG 2208

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 GTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2268

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 TATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAGGC 2328

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 GCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2388

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2448

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2508

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2568

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2628

Qy    801 LysProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2688

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2748

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2808

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2868

Qy    881 ValIle 882
          ||||||
Db   2869 GTGATA 2874

RESULT 6
AAH99935
ID   AAH99935 standard; cDNA; 2643 BP.
XX
AC   AAH99935;
XX
DT   12-APR-2002  (first entry)
XX
DE   Coding sequence of 21953 human prolyl oligopeptidase.
XX
KW   21953 prolyl oligopeptidase; antibody; proline; endopeptidase;
KW   cancer; cardiovascular disease; autoimmune disease; atopic allergy;
KW   neuronal disorder; vascular disorder; prostate disorder; cytostatic;
KW   antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
KW   diabetes mellitus; arthritis; multiple sclerosis; asthma;
KW   Grave's disease; neuronal disorder; demyelinating disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179473-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US40483.
XX
PR   18-APR-2000; 2000US-197508P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers RA,  Williamson M;
XX
DR   WPI; 2002-034353/04.
DR   P-PSDB; AAG78415.
XX
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PT New polypeptides 21953, member of human prolyl oligopeptidase family,
PT useful as diagnostic targets and therapeutic agents for controlling
PT cancer, lymphoma and leukemia -
XX
PS Claim 2; Page-; 121pp; English.
XX
CC This invention relates to an isolated 21953 human prolyl
CC oligopeptidase. Which is cytostatic, antidiabetic, antiarthritic,
CC neuroprotective, antithyroid, dermatological, antipsoriatic,
CC antiasthmatic, ophthalmological, antiinflammatory, nootropic,
CC antiparkinsonian, anticonvulsant, gynaecological, vasotropic,
CC antianginal, cardiant, antiatherosclerotic, anorectic and
CC metabolic in its action. Uses include gene therapy, expression or
CC activity of 21953 protein modulator, it is useful for identifying a
CC compound which binds to it and can be used in preventing, treating
CC or detecting a cellular proliferative or differentiative disorder.
CC The 21953 molecules can act as novel diagnostic targets and therapeutic
CC agents for controlling disorders associated with the aberrant activity
CC or degradation of peptide hormones e.g., disorders associated with cell
CC differentiation and proliferation such as cancer, immune function,
CC reproductive, neurological and cardiovascular function. The 21953
CC molecules are thus useful for treating and preventing cellular
CC proliferative and differentiative disorders, haematopoietic neoplastic
CC disorders, immune disorders such as autoimmune diseases, diabetes
CC mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
CC neuronal disorders, demyelinating diseases, vascular disorders and
CC metabolism or pain disorders. This sequence represents the cDNA
CC encoding sequence of 21953 human prolyl oligopeptidase. This
CC sequence represents the coding sequence of 21953, being the sequence
CC in between the start and the stop codon of the sequence represented in
CC AAH99934.
XX
SQ Sequence 2643 BP; 800 A; 514 C; 585 G; 744 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2643
Score:	4695.00	Matches:	881
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.89%	Indels:	0
DB:	24	Gaps:	0

US-10-070-464-1 (1-882) x AAH99935 (1-2643)

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Qy      2 AlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCysGlu 21
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGTGAG 60

Qy     22 GluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyrSer 41
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTATTCC 120

Qy     42 TrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMetAla 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATGGCT 180

Qy     62 LysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSerAsp 81
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCAGAC 240

Qy     82 ArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSerGlu 101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCTGAA 300

Qy    102 IleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeuAsp 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTGGAT 360

Qy    122 LeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArgGlu 141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGAGAA 420

Qy    142 ArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGlyThr 161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGAACA 480

Qy    162 PheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGlyPhe 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGATTT 540

Qy    182 ThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAsp 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATGGAT 600

Qy    202 ProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIleTrp 221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATTTGG 660

Qy    222 IleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeuAla 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTAGCC 720

Qy    242 AsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPhe 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAATTT 780

Qy    262 AspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGlyLys 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGTAAA 840

Qy    282 IleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisValThr 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTTACA 900

Qy    302 SerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThrAla 321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACAGCA 960

Qy    322 AsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIle 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATCATA 1020

Qy    342 AspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGluTyr 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAATAT 1080

Qy    362 IleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAspArg 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGATCGC 1140

Qy    382 SerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGluAsp 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCCCAGACTCGCCTGCAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAAGAT 1200

Qy    402 AspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeuIle 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTAATT 1260

Qy    422 IleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhePro 441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTTCCC 1320

Qy    442 GlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheArg 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTCCGT 1380

Qy    462 HisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGlyGly 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGTGGG 1440

Qy    482 LeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSerGly 501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGTGGT 1500

Qy    502 GluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArgLeu 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1501 GAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGGCTG 1560

Qy   522 ValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSerTyr 541
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGTTAC 1620

Qy   542 ValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCysIle 561
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGCATC 1680

Qy   562 SerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCysVal 581
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 AGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGTGTG 1740

Qy   582 SerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPheTrp 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTTTGG 1800

Qy   602 AlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePheSer 621
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTCTCT 1860

Qy   622 PheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeuGln 641
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTACAG 1920

Qy   642 ProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeuVal 661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAGGTGCAGTTGGTG 1980

Qy   662 AsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyr 681
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGTTAT 2040

Qy   682 ValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGlyAla 701
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 GTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAGGCGCC 2100

Qy   702 PheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyrLeu 721
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATATCTA 2160

Qy   722 AlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyrGly 741
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTATGGA 2220

Qy   742 GlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIleAla 761
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATTGCT 2280

Qy   762 GlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMetGly 781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 GGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATGGGT 2340

Qy   782 HisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGluLys 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAAAAG 2400

Qy   802 PheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnValHis 821
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTCCAT 2460

Qy   822 PheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAspLeu 841
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 TTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGATTTA 2520

Qy   842 GlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyrGlu 861
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTATGAA 2580

Qy   862 LeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLysVal 881
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAAGTG 2640
```

```
Qy    882 Ile 882
           |||
Db   2641 ATA 2643

RESULT 7
ABK83327
ID   ABK83327 standard; cDNA; 4829 BP.
XX
AC   ABK83327;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-1 splice variant #3.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61596.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 65-66; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4829 BP; 1466 A; 886 C; 1017 G; 1460 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          4829
Score:                    4680.00        Matches:         882
Percent Similarity:       99.77%         Conservative:    0
Best Local Similarity:    99.77%         Mismatches:      0
Query Match:              99.57%         Indels:          2
DB:                       24             Gaps:            0

US-10-070-464-1 (1-882) x ABK83327 (1-4829)
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Qy      1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy     21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr  40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy     41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy     61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy     81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy    101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy    121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy    141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy    161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy    181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy    201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy    221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy    241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy    261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy    281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy    301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy    321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293
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Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1713

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2014 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2073

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2074 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2133

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGly--ProGlnValGlnL 660
          |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db   2134 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCTCCTCAGGTGCAGT 2193

Qy    660 euValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuG 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2194 TGGTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAG 2253

Qy    680 lyTyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluG 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2254 GTTATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAG 2313

Qy    700 lyAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2314 GCGCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAAT 2373

Qy    720 yrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerT 740
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2374 ATCTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCT 2433

Qy     740 yrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaI 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2434 ATGGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTA 2493

Qy     760 leAlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrM 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2494 TTGCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATA 2553

Qy     780 etGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaG 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2554 TGGGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAG 2613

Qy     800 luLysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnV 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2614 AAAAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATG 2673

Qy     820 alHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2674 TCCATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATG 2733

Qy     840 spLeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisT 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2734 ATTTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATT 2793

Qy     860 yrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuL 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2794 ATGAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAA 2853

Qy     880 ysValIle 882
          ||||||||
Db    2854 AAGTGATA 2861

RESULT 8
ABK83332
ID   ABK83332 standard; cDNA; 4685 BP.
XX
AC   ABK83332;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-1 splice variant #8.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61601.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 75-76; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4685 BP; 1430 A; 853 C; 991 G; 1411 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          4685
Score:                    4385.50        Matches:         834
Percent Similarity:       94.56%         Conservative:    0
Best Local Similarity:    94.56%         Mismatches:      1
Query Match:              93.31%         Indels:          48
DB:                       24             Gaps:            1

US-10-070-464-1 (1-882) x ABK83332 (1-4685)

Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    814 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy    221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy    241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy    261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy    281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy    301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy    321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293

Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1713

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953
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Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
          ||||||||||||||||||||
Db   2014 TGGGCCACCATTTTGGATTCAGT---------------------------------- 2036

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640

Db   2036 ------------------------------------------------------------ 2036

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
                                                    ||||||||||||||||
Db   2037 ---------------------------------------------CCTCAGGTGCAGTTG 2051

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 GTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAGGT 2111

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 TATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAGGC 2171

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 GCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2231

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2291

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2351

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2411

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2471

Qy    801 LysProProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2531

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2591

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2651

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2711

Qy    881 ValIle 882
          ||||||
Db   2712 GTGATA 2717

RESULT 9
ABK83331
ID   ABK83331 standard; cDNA; 4676 BP.
XX
AC   ABK83331;
XX
DT   12-AUG-2002  (first entry)
XX
```

DE cDNA encoding human DPRP-1 splice variant #7.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61600.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 72-73; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4676 BP; 1424 A; 859 C; 979 G; 1414 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	4676
Score:	4385.00	Matches:	831
Percent Similarity:	94.22%	Conservative:	0
Best Local Similarity:	94.22%	Mismatches:	1
Query Match:	93.30%	Indels:	51
DB:	24	Gaps:	1

US-10-070-464-1 (1-882) x ABK83331 (1-4676)

```
Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
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Db   1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460

Db   1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480

Db   1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500

Db   1654 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1713

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520

Db   1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540

Db   1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560

Db   1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580

Db   1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600

Db   1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620

Db   2014 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2073

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640

Db   2074 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2133

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660

Db   2134 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCG---------- 2180

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680

Db   2180 ---------- 2180

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700

Db   2180 ---------- 2180

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

Db   2181 ----------GGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAATAT 2222

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740

Db   2223 CTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCTAT 2282

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760

Db   2283 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTATT 2342

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780

Db   2343 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2402

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800

Db   2403 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2462

Qy    801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820

Db   2463 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2522

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840

Db   2523 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2582

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860

Db   2583 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2642

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880

Db   2643 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2702

Qy    881 ValIle 882

Db   2703 GTGATA 2708
```

RESULT 10
ABN59774
ID ABN59774 standard; cDNA; 2842 BP.
XX
AC ABN59774;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 185.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR P-PSDB; ABB97361.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Claim 1; SEQ ID NO 185; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention.
XX
SQ Sequence 2842 BP; 857 A; 592 C; 635 G; 758 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2842
Score:	4118.00	Matches:	782
Percent Similarity:	88.66%	Conservative:	0
Best Local Similarity:	88.66%	Mismatches:	0
Query Match:	87.62%	Indels:	100
DB:	24	Gaps:	1

US-10-070-464-1 (1-882) x ABN59774 (1-2842)

```
Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys  20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 293

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 353

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 413

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 473

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 533

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 593

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 653

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     654 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 713

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     714 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 773

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     774 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 833

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     834 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 893

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     894 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 953

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     954 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 1013

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1014 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1073

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1133

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1134 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1193

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1194 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1253

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1254 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1313

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1314 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1373

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1374 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1433

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1493

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1494 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1553

Qy     441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1554 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1613

Qy     461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1614 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1673

Qy     481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1674 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1733

Qy     501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1734 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1793

Qy     521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1794 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1853

Qy     541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1854 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1913

Qy     561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1914 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1973

Qy     581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1974 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2033

Qy     601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2034 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2093

Qy     621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2094 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2153

Qy     641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2154 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAG--------- 2204

Qy     661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680

Db    2204 ---------------------------------------------------------- 2204
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Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700

Db   2204 ------------------------------------------------------------ 2204

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

Db   2204 ------------------------------------------------------------ 2204

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740

Db   2204 ------------------------------------------------------------ 2204

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
                                                        |||||||||
Db   2205 ----------------------------------------------GTTGCTATT 2213

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2273

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2333

Qy    801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2334 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2393

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2394 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2453

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2454 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2513

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2514 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2573

Qy    881 ValIle 882
          ||||||
Db   2574 GTGATA 2579

RESULT 11
ABK83325
ID   ABK83325 standard; cDNA; 4523 BP.
XX
AC   ABK83325;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-1 splice variant #1.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61594.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 61-62; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4523 BP; 1384 A; 828 C; 940 G; 1371 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          4523
Score:                    4092.50        Matches:         780
Percent Similarity:       88.44%         Conservative:    0
Best Local Similarity:    88.44%         Mismatches:      1
Query Match:              87.07%         Indels:          102
DB:                       24             Gaps:            1

US-10-070-464-1 (1-882) x ABK83325 (1-4523)

Qy      1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273

Qy     21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy     41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy     61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy     81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy    101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy    121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy    141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693
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Qy    161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy    181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy    201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy    221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy    241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy    261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy    281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy    301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy    321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1233

Qy    341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1293

Qy    361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1353

Qy    381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1413

Qy    401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1473

Qy    421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1533

Qy    441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1593

Qy    461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1653

Qy    481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1713

Qy    501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1773

Qy    521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1833

Qy    541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1893

Qy    561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1953

Qy    581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 2013

Qy    601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2014 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 2073

Qy    621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2074 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 2133

Qy    641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2134 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGT---------------- 2178

Qy    661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680

Db   2178 ---------------------------------------------------------- 2178

Qy    681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700

Db   2178 ---------------------------------------------------------- 2178

Qy    701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

Db   2178 ---------------------------------------------------------- 2178

Qy    721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740

Db   2178 ---------------------------------------------------------- 2178

Qy    741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
                                                        |||   ||||||
Db   2179 ----------------------------------------------CGGTT-GCTATT 2189

Qy    761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2249

Qy    781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2250 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2309

Qy    801 LysProProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2310 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2369

Qy    821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2429

Qy    841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2489

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2549

Qy    881 ValIle 882
          ||||||
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Db   2550 GTGATA 2555

RESULT 12
AAD23843
ID   AAD23843 standard; cDNA; 2510 BP.
XX
AC   AAD23843;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Human protease PRTS-2 cDNA.
XX
KW   Human; protease; PRTS-2; tranquilliser; gene therapy; vaccine; allergy;
KW   infection; dermatitis; arteriosclerosis; rheumatoid arthritis; hepatitis;
KW   atherosclerosis; psoriasis; Alzheimer's disease; mental disorder; cancer;
KW   gastrointestinal disorder; Cushing's syndrome; seizure; glaucoma; stroke;
KW   epithelial disorder; urticaria; anorexia; trauma; asthma; eczema; nausea;
KW   hypertension; neurological disorder; Parkinson's disease; drug screening;
KW   cardiant; cell proliferative disorder; multiple sclerosis; osteoporosis;
KW   diabetes mellitus; glomerulonephritis; cardiovascular disorder; anaemia;
KW   autoimmune disorder; inflammatory disorder; myocardial infarction; AIDS;
KW   developmental disorder; reproductive disorder; infertility; diarrhoea;
KW   dementia; acidosis; cataract; gynaecomastia; epilepsy; jaundice; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             616..2358
FT                   /*tag= a
FT                   /product= "Human protease PRTS-2 protein"
XX
PN   WO200183775-A2.
XX
PD   08-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US14651.
XX
PR   04-MAY-2000; 2000US-202082P.
PR   11-MAY-2000; 2000US-203566P.
PR   17-MAY-2000; 2000US-205803P.
PR   25-MAY-2000; 2000US-207477P.
PR   01-JUN-2000; 2000US-209402P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Delegeane AM,  Lal P,  Hafalia A,  Patterson C,  Walia NK,  Kearney L;
PI   Tribouley CM,  Khan FA,  Yao MG,  Baughn MR,  Azimzai Y,  Elliott VS;
PI   Nguyen DB,  Gandhi AR,  Yang J,  Hernandez R,  Policky JL,  Lu DAM;
PI   Reddy R,  Yue H,  Tang YT;
XX
DR   WPI; 2002-034518/04.
DR   P-PSDB; AAE14337.
XX
PT   Novel human proteases and polynucleotides encoding the proteases,
PT   useful for treating, diagnosing or preventing cell proliferative,
PT   cardiovascular, autoimmune/inflammatory, neurological and developmental
PT   disorders -
XX
PS   Claim 5; Page 139-140; 151pp; English.
XX
CC   The invention relates to human proteases (PRTS1-14) and its corresponding
CC   cDNA molecules. Human PRTS and its nucleic acid molecule are useful for
CC   the diagnosis, treatment and prevention of disorders associated with
CC   increased or decreased expression of PRTS. Examples of such disorders
CC   include, cell proliferative disorders (arteriosclerosis, atherosclerosis,
CC   hepatitis, psoriasis and cancers); autoimmune/inflammatory disorders
CC   (AIDS, Addison's disease, allergy, anaemia, asthma, atopic dermatitis,
CC   diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoporosis,
CC   trauma, Grave's disease, rheumatoid arthritis, ulcerative colitis, and
CC   viral, bacterial, fungal, parasitic, protozoal and helminthic
CC   infections); cardiovascular disorders (myocardial infarction, ischaemic
CC   heart disease and hypertension); neurological disorders (epilepsy,
CC   Alzheimer's disease, Pick's disease, Huntington's disease, dementia,
CC   Parkinson's disease, stroke, mental disorders including mood, anxiety
CC   and seasonal affective disorder and prion diseases); gastrointestinal
CC   disorders (Crohn's disease, anorexia, nausea, diarrhoea and jaundice);
CC   epithelial disorders (contact dermatitis, eczema, acne vulgaris,
CC   alopecia, scabies, insect bites and urticaria); reproductive disorder
CC   (infertility, disruption of estrous and menstrual cycle and
CC   gynaecomastia); and developmental disorders (renal tubular acidosis,
CC   Cushing's syndrome, seizure disorders, congenital glaucoma and cataract).
CC   PRTS DNA is also in useful is gene therapy. PRTS and its immunogenic
CC   fragments are useful for screening libraries of compounds in several drug
CC   screening assays. The present sequence is human protease PRTS-2 cDNA.
XX
SQ   Sequence 2510 BP; 777 A; 494 C; 527 G; 712 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2510
Score:                    3970.50        Matches:         764
Percent Similarity:       89.81%         Conservative:    3
Best Local Similarity:    89.46%         Mismatches:      5
Query Match:              84.48%         Indels:          82
DB:                       24             Gaps:            6

US-10-070-464-1 (1-882) x AAD23843 (1-2510)

Qy     42 TrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMetAla 61
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 TGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATGGCT 62

Qy     62 LysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSerAsp 81
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 AAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCAGAC 122

Qy     82 ArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSerGlu 101
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 AGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCTGAA 182

Qy    102 IleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeuAsp 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 ATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTGGAT 242

Qy    122 LeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArgGlu 141
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 CTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGAGAA 302

Qy    142 ArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGlyThr 161
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 AGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGAACA 362

Qy    162 PheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGlyPhe 181
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 TTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGATTT 422

Qy    182 ThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAsp 201
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 ACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATGGAT 482

Qy    202 ProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIleTrp 221
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 CCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATTTGG 542

Qy    222 IleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeuAla 241
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 ATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTAGCC 602

Qy    242 AsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPhe 261
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 AACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAATTT 662

Qy    262 AspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGlyLys 281
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 GATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGTAAA 722

Qy    282 IleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisValThr 301
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Db    723 ATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTTACA 782

Qy    302 SerProMetLeuGluThrArg-ArgAlaAspSerPheArgTyrProLysThrGlyThrAl 321
Db    783 TCCCCTATGTTGGAAACAAGGCAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACAGC 842

Qy    321 aAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIl 341
Db    843 AAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATCAT 902

Qy    341 eAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGluTy 361
Db    903 AGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAATA 962

Qy    361 rIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAspAr 381
Db    963 TATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGATCG 1022

Qy    381 gSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGluAs 401
Db   1023 CTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAAGA 1082

Qy    401 pAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeuIl 421
Db   1083 TGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTAAT 1142

Qy    421 eIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhePr 441
Db   1143 TATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTTCC 1202

Qy    441 oGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheAr 461
Db   1203 CCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTCCG 1262

Qy    461 gHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGlyGl 481
Db   1263 TCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGTGG 1322

Qy    481 yLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSerGl 501
Db   1323 GCTGCCTGCTCCAACT----------------------------------GTCACT----- 1344

Qy    501 yGluTrpGluVal---------------LeuGly----------------------ArgHi 509
Db   1345 ----TGGATGATCACATTCATGAGATCTCTAGGAACTCCATCCTGTATGTGTGTGACACA 1400

Qy    509 sGlySerAsnIleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAs 529
Db   1401 TATAGTTGAGATCCAAGTTGATGAAGTCAGAAGGCTGGTATATTTTGAAGGCACCAAAGA 1460

Qy    529 pSerProLeuGluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrAr 549
Db   1461 CTCCCCTTTAGAGCATCACCTGTACGTAGTCAGTTACGTAAATCCTGGAGAGGTGACAAG 1520

Qy    549 gLeuThrAspArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIl 569
Db   1521 GCTGACTGACCGTGGCTACTCACATTCTTGCTGCATCAGTCAGCACTGTGACTTCTTTAT 1580

Qy    569 eSerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerPr 589
Db   1581 AAGTAAGTATAGTAACCAGAAGAATCCACACTGTGTGTCCCTTTACAAGCTATCAAGTCC 1640

Qy    589 oGluAspAspProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGl 609
Db   1641 TGAAGATGACCCAACTTGCAAAACAAAGGAATTTTGGGCCACCATTTTGGATTCAGCAGG 1700

Qy    609 yProLeuProAspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheTh 629
Db   1701 TCCTCTTCCTGACTATACTCCTCCAGAAATTTTCTCTTTTGAAAGTACTACTGGATTTAC 1760

Qy    629 rLeuTyrGlyMetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrVa 649
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Db   1761 ATTGTATGGGATGCTCTACAAGCCTCATGATCTACAGCCTGGAAAGAAATATCCTACTGT 1820

Qy    649 lLeuPheIleTyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLy 669
Db   1821 GCTGTTCATATATGGTGGTCCTCAGGTGCAGTTGGTGAATAATCGGTTTAAAGGAGTCAA 1880

Qy    669 sTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnAr 689
Db   1881 GTATTTCCGCTTGAATACCCTAGCCTCTCTAGGTTATGTGGTTGTAGTGATAGACAACAG 1940

Qy    689 gGlySerCysHisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIl 709
Db   1941 GGGATCCTGTCACCGAGGGCTTAAATTTGAAGGCGCCTTTAAATATAAAATG-------- 1992

Qy    709 eGluIleAspAspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAs 729
Db   1992 ---------------------------------------------------------- 1992

Qy    729 pLeuAspArgValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLe 749
Db   1992 ---------------------------------------------------------- 1992

Qy    749 uMetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIl 769
Db   1993 ------------------------GTTGCTATTGCTGGGGCCCCAGTCACTCTGTGGAT 2027

Qy    769 ePheTyrAspThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGl 789
Db   2028 CTTCTATGATACAGGATACACGGAACGTTATATGGGTCACCCTGACCAGAATGAACAGGG 2087

Qy    789 yTyrTyrLeuGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLe 809
Db   2088 CTATTACTTAGGATCTGTGGCCATGCAAGCAGAAAAGTTCCCCTCTGAACCAAATCGTTT 2147

Qy    809 uLeuLeuLeuHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLe 829
Db   2148 ACTGCTCTTACATGGTTTCCTGGATGAGAATGTCCATTTTGCACATACCAGTATATTACT 2207

Qy    829 uSerPheLeuValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHi 849
Db   2208 GAGTTTTTTAGTGAGGGCTGGAAAGCCATATGATTTA-----------CAGGAGAGACA 2255

Qy    849 sSerIleArgValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGl 869
Db   2256 CAGCATAAGAGTTCCTGAATCGGGAGAACATTATGAACTGCATCTTTTGCACTACCTTCA 2315

Qy    869 nGluAsnLeuGlySerArgIleAlaAlaLeuLysValIle 882
Db   2316 AGAAAACCTTGGATCACGTATTGCTGCTCTAAAAGTGATA 2355

RESULT 13
ABN59775
ID   ABN59775 standard; cDNA; 2668 BP.
XX
AC   ABN59775;
XX
DT   28-JUN-2002  (first entry)
XX
DE   Novel human coding sequence SEQ ID NO: 186.
XX
KW   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW   antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW   neuroprotective; antiparkinsonian; protein therapy; EST;
KW   expressed sequence tag; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222660-A2.
XX
PD   21-MAR-2002.
XX
PF   10-SEP-2001; 2001WO-US26015.
XX
```

PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR P-PSDB; ABB97362.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Claim 1; SEQ ID NO 186; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention.
XX
SQ Sequence 2668 BP; 796 A; 564 C; 592 G; 716 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2668
Score:	3771.00	Matches:	724
Percent Similarity:	82.09%	Conservative:	0
Best Local Similarity:	82.09%	Mismatches:	0
Query Match:	80.23%	Indels:	158
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x ABN59775 (1-2668)

```
Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 293

Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 353

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 413

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 473

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 533

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 593

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
           ||||||||||||
Db     594 GATCTTTTTCAG---------------------------------------------- 605

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160

Db     605 ---------------------------------------------------------- 605

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180

Db     605 ---------------------------------------------------------- 605

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     606 ------CAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 659

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 719

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 779

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 839

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 899

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 959

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1019

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGGATC 1079

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080 ATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATTCTATTTGAAGGAGTTGAA 1139

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 TATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCTTGGTCCATCCTACTAGAT 1199

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 CGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAATTATTTATCCCAGTAGAA 1259

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 GATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCTGATTCTGTGACGCCACTA 1319

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 ATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCATGACATCTTTCATGTTTTT 1379

Qy     441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 CCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCTGAATGCAAAACAGGTTTC 1439

Qy     461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 CGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAATATAAACGATCCAGTGGT 1499

Qy     481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1500 GGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAGGAGATAGCAATTACCAGT 1559

Qy     501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1560 GGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAAGTTGATGAAGTCAGAAGG 1619

Qy     521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1620 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1679
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Qy     541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1680 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1739

Qy     561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1740 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1799

Qy     581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1800 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 1859

Qy     601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1860 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 1919

Qy     621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1920 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 1979

Qy     641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1980 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCCTCAG--------- 2030

Qy     661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680

Db    2030 ------------------------------------------------------------ 2030

Qy     681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700

Db    2030 ------------------------------------------------------------ 2030

Qy     701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

Db    2030 ------------------------------------------------------------ 2030

Qy     721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyr 740

Db    2030 ------------------------------------------------------------ 2030

Qy     741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
                                                          |||||||||
Db    2031 ----------------------------------------------------GTTGCTATT 2039

Qy     761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2040 GCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATATG 2099

Qy     781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2100 GGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAGAA 2159

Qy     801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2160 AAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTC 2219

Qy     821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2220 CATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATGAT 2279

Qy     841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2280 TTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATTAT 2339

Qy     861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2340 GAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAAAA 2399

Qy     881 ValIle 882
           ||||||
Db    2400 GTGATA 2405
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RESULT 14
ABK83328
ID   ABK83328 standard; cDNA; 4309 BP.
XX
AC   ABK83328;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-1 splice variant #4.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61597.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 67-68; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4309 BP; 1304 A; 790 C; 907 G; 1308 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          4309
Score:                    3661.50        Matches:         708
Percent Similarity:       80.09%         Conservative:    0
Best Local Similarity:    80.09%         Mismatches:      1
Query Match:              77.90%         Indels:          176
DB:                       24             Gaps:            1

US-10-070-464-1 (1-882) x ABK83328 (1-4309)

Qy       1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 ATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTTGAGATATTTGAAACTGCGGACTGT 273
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Qy      21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GAGGAGAATATTGAATCACAGGATCGGCCTAAATTGGAGCCTTTTTATGTTGAGCGGTAT 333

Qy      41 SerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 TCCTGGAGTCAGCTTAAAAAGCTGCTTGCCGATACCAGAAAATATCATGGCTACATGATG 393

Qy      61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTAAGGCACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCA 453

Qy      81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 GACAGAATCTATTACCTTGCCATGTCTGGTGAGAACAGAGAAAATACACTGTTTTATTCT 513

Qy     101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GAAATTCCCAAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAAGCCTCTTTTG 573

Qy     121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuLeuArg 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GATCTTTTTCAGGCAACACTGGACTATGGAATGTATTCTCGAGAAGAAGAACTATTAAGA 633

Qy     141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GAAAGAAAACGCATTGGAACAGTCGGAATTGCTTCTTACGATTATCACCAAGGAAGTGGA 693

Qy     161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 ACATTTCTGTTTCAAGCCGGTAGTGGAATTTATCACGTAAAAGATGGAGGGCCACAAGGA 753

Qy     181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 TTTACGCAACAACCTTTAAGGCCCAATCTAGTGGAAACTAGTTGTCCCAACATACGGATG 813

Qy     201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 GATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTTATACATAGCAACGATATT 873

Qy     221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 TGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACTTATGTGCACAATGAGCTA 933

Qy     241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 GCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACCTTTGTTCTCCAAGAAGAA 993

Qy     261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 TTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAAACAACTCCCAGTGGTGGT 1053

Qy     281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1054 AAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAGGTGGAAATTATTCATGTT 1113

Qy     301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 ACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGTTATCCTAAAACAGGTACA 1173

Qy     321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 GCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATTGATGCTGAAGGAAGATC- 1232

Qy     341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360

Db    1232 ------------------------------------------------------------ 1232

Qy     361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380

Db    1232 ------------------------------------------------------------ 1232

Qy     381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
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Db    1232 ------------------------------------------------------------ 1232

Qy     401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420

Db    1232 ------------------------------------------------------------ 1232

Qy     421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440

Db    1232 ------------------------------------------------------------ 1232

Qy     441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460

Db    1232 ------------------------------------------------------------ 1232

Qy     461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480

Db    1232 ------------------------------------------------------------ 1232

Qy     481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500

Db    1232 ------------------------------------------------------------ 1232

Qy     501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
                                                   ||||||||||||||||||||
Db    1233 ------------------------------------CAAGTTGATGAAGTCAGAAGG 1253

Qy     521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1254 CTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCATCACCTGTACGTAGTCAGT 1313

Qy     541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1314 TACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTGGCTACTCACATTCTTGCTGC 1373

Qy     561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1374 ATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAACCAGAAGAATCCACACTGT 1433

Qy     581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 GTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACTTGCAAAACAAAGGAATTT 1493

Qy     601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1494 TGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTATACTCCTCCAGAAATTTTC 1553

Qy     621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1554 TCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTCTACAAGCCTCATGATCTA 1613

Qy     641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGly--ProGlnValGlnL 660
           |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db    1614 CAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGTGGTCTCCTCAGGTGCAGT 1673

Qy     660 euValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuG 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1674 TGGTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAATACCCTAGCCTCTCTAG 1733

Qy     680 lyTyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluG 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1734 GTTATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGAGGGCTTAAATTTGAAG 1793

Qy     700 lyAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1794 GCGCCTTTAAATATAAAATGGGTCAAATAGAAATTGACGATCAGGTGGAAGGACTCCAAT 1853

Qy     720 yrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerT 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1854 ATCTAGCTTCTCGATATGATTTCATTGACTTAGATCGTGTGGGCATCCACGGCTGGTCCT 1913

Qy     740 yrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaI 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   1914 ATGGAGGATACCTCTCCCTGATGGCATTAATGCAGAGGTCAGATATCTTCAGGGTTGCTA 1973

Qy    760 leAlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrM 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 TTGCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGATACACGGAACGTTATA 2033

Qy    780 etGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaG 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2034 TGGGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCTGTGGCCATGCAAGCAG 2093

Qy    800 luLysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnV 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2094 AAAAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATG 2153

Qy    820 alHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 TCCATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGGGCTGGAAAGCCATATG 2213

Qy    840 spLeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisT 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 ATTTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCTGAATCGGGAGAACATT 2273

Qy    860 yrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuL 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 ATGAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCACGTATTGCTGCTCTAA 2333

Qy    880 ysValIle 882
          ||||||||
Db   2334 AAGTGATA 2341

RESULT 15
AAH15009
ID   AAH15009 standard; cDNA; 2161 BP.
XX
AC   AAH15009;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:12963.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 12963; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2161 BP; 662 A; 429 C; 452 G; 618 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2161
Score:                    3364.50        Matches:         636
Percent Similarity:       92.44%         Conservative:    0
Best Local Similarity:    92.44%         Mismatches:      1
Query Match:              71.59%         Indels:          51
DB:                       22             Gaps:            1

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Qy    195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGTCCCAACATACGGATGGATCCAAAATTATGCCCTGCTGATCCAGACTGGATTGCTTTT 60

Qy    215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATACATAGCAACGATATTTGGATATCTAACATCGTAACCAGAGAAGAAAGGAGACTCACT 120

Qy    235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TATGTGCACAATGAGCTAGCCAACATGGAAGAAGATGCCAGATCAGCTGGAGTCGCTACC 180

Qy    255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTTGTTCTCCAAGAAGAATTTGATAGATATTCTGGCTATTGGTGGTGTCCAAAAGCTGAA 240

Qy    275 ThrThrProSerGlyGlyLysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGlu 294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACAACTCCCAGTGGTGGTAAAATTCTTAGAATTCTATATGAAGAAAATGATGAATCTGAG 300

Qy    295 ValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPheArg 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGAAATTATTCATGTTACATCCCCTATGTTGGAAACAAGGAGGGCAGATTCATTCCGT 360

Qy    315 TyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMetIle 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TATCCTAAAACAGGTACAGCAAATCCTAAAGTCACTTTTAAGATGTCAGAAATAATGATT 420

Qy    335 AspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGluIle 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GATGCTGAAGGAAGGATCATAGATGTCATAGATAAGGAACTAATTCAACCTTTTGAGATT 480

Qy    355 LeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAla 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTATTTGAAGGAGTTGAATATATTGCCAGAGCTGGATGGACTCCTGAGGGAAAATATGCT 540

Qy    375 TrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerProGlu 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGTCCATCCTACTAGATCGCTCCCAGACTCGCCTACAGATAGTGTTGATCTCACCTGAA 600

Qy    395 LeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerValPro 414
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Db    601 TTATTTATCCCAGTAGAAGATGATGTTATGGAAAGGCAGAGACTCATTGAGTCAGTGCCT 660

Qy    415 AspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIleHis 434

Db    661 GATTCTGTGACGCCACTAATTATCTATGAAGAAACAACAGACATCTGGATAAATATCCAT 720

Qy    435 AspIlePheHisValPheProGlnSerHisGluGluGluIleGluPheIlePheAlaSer 454

Db    721 GACATCTTTCATGTTTTTCCCCAAAGTCACGAAGAGGAAATTGAGTTTATTTTTGCCTCT 780

Qy    455 GluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLys 474

Db    781 GAATGCAAAACAGGTTTCCGTCATTTATACAAAATTACATCTATTTTAAAGGAAAGCAAA 840

Qy    475 TyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIleLysGlu 494

Db    841 TATAAACGATCCAGTGGTGGGCTGCCTGCTCCAAGTGATTTCAAGTGTCCTATCAAAGAG 900

Qy    495 GluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGln 514

Db    901 GAGATAGCAATTACCAGTGGTGAATGGGAAGTTCTTGGCCGGCATGGATCTAATATCCAA 960

Qy    515 ValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeuGluHis 534

Db    961 GTTGATGAAGTCAGAAGGCTGGTATATTTTGAAGGCACCAAAGACTCCCCTTTAGAGCAT 1020

Qy    535 HisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAspArgGly 554

Db   1021 CACCTGTACGTAGTCAGTTACGTAAATCCTGGAGAGGTGACAAGGCTGACTGACCGTAGC 1080

Qy    555 TyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyrSerAsn 574

Db   1081 TACTCACATTCTTGCTGCATCAGTCAGCACTGTGACTTCTTTATAAGTAAGTATAGTAAC 1140

Qy    575 GlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAspProThr 594

Db   1141 CAGAAGAATCCACACTGTGTGTCCCTTTACAAGCTATCAAGTCCTGAAGATGACCCAACT 1200

Qy    595 CysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyr 614

Db   1201 TGCAAAACAAAGGAATTTTGGGCCACCATTTTGGATTCAGCAGGTCCTCTTCCTGACTAT 1260

Qy    615 ThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeu 634

Db   1261 ACTCCTCCAGAAATTTTCTCTTTTGAAAGTACTACTGGATTTACATTGTATGGGATGCTC 1320

Qy    635 TyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIleTyrGly 654

Db   1321 TACAAGCCTCATGATCTACAGCCTGGAAAGAAATATCCTACTGTGCTGTTCATATATGGT 1380

Qy    655 GlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsn 674

Db   1381 GGTCCTCAGGTGCAGTTGGTGAATAATCGGTTTAAAGGAGTCAAGTATTTCCGCTTGAAT 1440

Qy    675 ThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCysHisArg 694

Db   1441 ACCCTAGCCTCTCTAGGTTATGTGGTTGTAGTGATAGACAACAGGGGATCCTGTCACCGA 1500

Qy    695 GlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGln 714

Db   1501 GGGCTTAAATTTGAAGGCGCCTTTAAATATAAAATG---------- 1536

Qy    715 ValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGly 734

Db   1536 ---------- 1536

Qy    735 IleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAsp 754

Db   1536 ---------- 1536

Qy    755 IlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGly 774

Db   1537 ---------GTTGCTATTGCTGGGGCCCCAGTCACTCTGTGGATCTTCTATGATACAGGA 1587

Qy    775 TyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySer 794

Db   1588 TACACGGAACGTTATATGGGTCACCCTGACCAGAATGAACAGGGCTATTACTTAGGATCT 1647

Qy    795 ValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuLeuHisGly 814

Db   1648 GTGGCCATGCAAGCAGAAAAGTTCCCCTCTGAACCAAATCGTTTACTGCTCTTACATGGT 1707

Qy    815 PheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArg 834

Db   1708 TTCCTGGATGAGAATGTCCATTTTGCACATACCAGTATATTACTGAGTTTTTTAGTGAGG 1767

Qy    835 AlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArgValPro 854

Db   1768 GCTGGAAAGCCATATGATTTACAGATCTATCCTCAGGAGAGACACAGCATAAGAGTTCCT 1827

Qy    855 GluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySer 874

Db   1828 GAATCGGGAGAACATTATGAACTGCATCTTTTGCACTACCTTCAAGAAAACCTTGGATCA 1887

Qy    875 ArgIleAlaAlaLeuLysValIle 882

Db   1888 CGTATTGCTGCTCTAAAAGTGATA 1911
```

RESULT 16
ABK83323
ID ABK83323 standard; cDNA; 2617 BP.
XX
AC ABK83323;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPPIV related serine protease DPRP-2.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61592.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Claim 1; Page 56-57; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly

CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 2617 BP; 558 A; 830 C; 736 G; 493 T; 0 other;

Alignment Scores:

Pred. No.:	4.04e-283	Length:	2617
Score:	2870.00	Matches:	517
Percent Similarity:	77.50%	Conservative:	134
Best Local Similarity:	61.55%	Mismatches:	187
Query Match:	61.06%	Indels:	2
DB:	24	Gaps:	2

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```
Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
Db      80 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 139

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
Db     140 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 199

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
Db     200 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 259

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
Db     260 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 319

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
Db     320 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 379

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
Db     380 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 439

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
Db     440 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGTCGC 499

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
Db     500 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 559

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
Db     560 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 619

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
Db     620 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 679

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
Db     680 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 739

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
Db     740 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 799

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
Db     800 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 859

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
Db     860 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 919

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
Db     920 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 979

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
Db     980 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1039

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
Db    1040 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1099

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
Db    1100 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1159

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
Db    1160 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1219

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
Db    1220 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1279

Qy     434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
Db    1280 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1339

Qy     453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db    1340 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1399

Qy     473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db    1400 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1459

Qy     493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db    1460 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCCAAG 1519

Qy     513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db    1520 ATCTGGGTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGACACGCCGCTG 1579

Qy     533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db    1580 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1639

Qy     553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db    1640 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 1699

Qy     573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db    1700 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 1759

Qy     593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db    1760 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 1819

Qy     613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db    1820 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 1879

Qy     633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db    1880 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 1939
```

```
Qy     653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
           ||||||||||||||||||||||||||||||||  ||||||||||:::||||||   |||
Db    1940 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 1999

Qy     673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
           ||||||||||||||||||||||||  ||||||||||||||  ||||||||||||
Db    2000 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2059

Qy     693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
           |||||||||:::||||||||||||   |||   :::||||||||||:::||||||::::
Db    2060 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2119

Qy     713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
           ||||||||||||||||||||:::::|||  ':::|||  ||||||||||||   |||
Db    2120 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2179

Qy     733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
           |||  ||||||||||||||||||||||:::||||||||||||  |||:::  :::
Db    2180 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2239

Qy     753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
           :::|||:::|||||||||||||||||||||||||||||:::|||:::  ||||||
Db    2240 CCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATGGCCTACGAC 2299

Qy     773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
           ||||||||||||||||||||||  |||:::  |||:::  ||||||
Db    2300 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2359

Qy     793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
           ||||||||||::  '||||||  |||:::|||||||||||||||||:::|||
Db    2360 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2419

Qy     813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
           ||||||||||||||||||||||||||  ||||||:::  |||:::|||  |||
Db    2420 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2479

Qy     833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
           :::||||||||||||||||  ||||||||||||||  ||||||||||||||||||
Db    2480 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2539

Qy     853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
           ||||||||||||||||||||||||:::  ||||||||:::|||||||||  |||
Db    2540 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2599

RESULT 17
ABK83335
ID   ABK83335 standard; cDNA; 4219 BP.
XX
AC   ABK83335;
XX
DT   12-AUG-2002 (first entry)
XX
DE   cDNA encoding human DPRP-2 splice variant #3.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61604.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 84-85; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4219 BP; 908 A; 1320 C; 1190 G; 801 T; 0 other;

Alignment Scores:
Pred. No.:              8.4e-283        Length:         4219
Score:                  2870.00         Matches:        517
Percent Similarity:     77.50%          Conservative:   134
Best Local Similarity:  61.55%          Mismatches:     187
Query Match:            61.06%          Indels:         2
DB:                     24              Gaps:           2

US-10-070-464-1 (1-882) x ABK83335 (1-4219)

Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||   |||:::::::::|||||      |||:::   ::::::      :::||||||
Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||   |||   ::::::   ||||||||||||||||||   ||||||::::::   |||
Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           ||||||||||||   |||:::||||||||||   |||         :::||||||
Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||   ||||||||||||||||||   :::   :::   |||:::|||:::|||
Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||   :::||||||   ||||||||||||       :::|||:::||||||||
Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           ||||||||||||||||||||||||||||||:::|||      ||||||   |||||||||
Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||   ||||||||||||||   :::   :::::::|||   :::
Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||      ||||||         |||:::::::|||      :::::::|||
Db     856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
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Db    916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy    215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234

Db    976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy    235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254

Db   1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy    255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274

Db   1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy    275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293

Db   1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy    294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313

Db   1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy    314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333

Db   1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy    334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353

Db   1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy    354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373

Db   1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy    374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393

Db   1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy    394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413

Db   1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy    414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433

Db   1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy    434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452

Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472

Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755

Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492

Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512

Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCCAAG 1875

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532

Db   1876 ATCTGGGTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGACACGCCGCTG 1935

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552

Db   1936 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1995

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
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Db   1996 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2055

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592

Db   2056 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2115

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612

Db   2116 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2175

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632

Db   2176 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2235

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652

Db   2236 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2295

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672

Db   2296 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2355

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692

Db   2356 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2415

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712

Db   2416 CAGCGAGGGCTTCGGTTCGAAGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2475

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732

Db   2476 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2535

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752

Db   2536 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2595

Qy    753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772

Db   2596 CCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATGGCCTACGAC 2655

Qy    773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792

Db   2656 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2715

Qy    793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812

Db   2716 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2775

Qy    813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832

Db   2776 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2835

Qy    833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852

Db   2836 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2895

Qy    853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872

Db   2896 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2955
```

RESULT 18
ABK83333
ID ABK83333 standard; cDNA; 4302 BP.
XX
AC ABK83333;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-2 splice variant #1.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;

KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61602.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 78-79; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4302 BP; 923 A; 1350 C; 1221 G; 808 T; 0 other;

Alignment Scores:

Pred. No.:	8.66e-283	Length:	4302
Score:	2870.00	Matches:	517
Percent Similarity:	77.50%	Conservative:	134
Best Local Similarity:	61.55%	Mismatches:	187
Query Match:	61.06%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x ABK83333 (1-4302)

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Qy     35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
          |||   |||:::::::::|||||      |||:::   ::::::      :::||||||
Db    436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy     55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
          |||   |||   ::::::   |||||||||||||||||   ||||||::::::   |||
Db    496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy     75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
          ||||||||||||   |||:::|||||||||   |||          :::|||||||
Db    556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy     95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
          |||:::|||   ||||||||||||||||||   :::   :::   |||:::|||:::|||
Db    616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy    115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
          |||||||||   :::||||||   ||||||||||||      :::|||:::|||||||||
Db    676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy    135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
          |||||||||||||||||||||||||||||:::|||      ||||||   |||||||||
Db    736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy    155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
          :::|||      ||||||   ||||||||||||||   :::   ::::::|||   :::
Db    796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy    175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
          |||||||||      ||||||         |||:::::::|||      :::::::|||
Db    856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915

Qy    195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
          |||         ||||||||||||||:::|||||||||||||||   :::   :::|||
Db    916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy    215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
          |||:::::::::|||:::|||:::::|||||   |||   ||||||||||||||||||
Db    976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy    235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
          :::   |||      |||:::|||:::   :::|||   :::||||||||||||||||||
Db   1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy    255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
          ||||||:::|||||||||||||||||||:::::|||||||||||||||||||   |||
Db   1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy    275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
                ||.|   |||   |||   ||||||||||||||||||||   |||||||||
Db   1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy    294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
          |||||||||:::|||||||||   ||||||   ||||||   |||:::   ||||||:::
Db   1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy    314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
          |||||||||:::|||||:::   ||||||||:::      |||:::::::|||
Db   1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy    334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
             |||:::::|||:::|||:::          :::|||||||||:::|||||||||
Db   1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy    354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
          ||||||      ||||||||||||||||||||||||||||||   :::|||||||||
Db   1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy    374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
          ||||||::::::   |||||||||   |||      ||||||:::|||||||:::   |||
Db   1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy    394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
          |||||||||||      ::::::      :::|||                  :::|||
Db   1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy    414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
          |||   :::|||   |||   :::::::|||||||||   |||:::::::|||||||:::
Db   1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy    434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
          ||||||||||||:::   ||||||||||||      |||:::|||:::   |||:::
Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
          |||:::|||||||||||||||||   ||||||||||||:::|||:::::|||||||
Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755
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Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCCAAG 1875

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db   1876 ATCTGGGTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGACACGCCGCTG 1935

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db   1936 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1995

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db   1996 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2055

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db   2056 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2115

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db   2116 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2175

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db   2176 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2235

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db   2236 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2295

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db   2296 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2355

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db   2356 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2415

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db   2416 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2475

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db   2476 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2535

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db   2536 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2595

Qy    753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
Db   2596 CCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATGGCCTACGAC 2655

Qy    773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
Db   2656 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2715

Qy    793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
Db   2716 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2775

Qy    813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db   2776 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2835

Qy    833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
```

```
Db   2836 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2895

Qy    853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
Db   2896 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2955
```

RESULT 19
AAD38954
ID AAD38954 standard; cDNA; 3024 BP.
XX
AC AAD38954;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human dipeptidyl peptidase 9 (DPP9) cDNA.
XX
KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..2910
FT   /*tag= a
FT   /product= "Human DPP9 protein"
FT   /transl_except= (pos: 1120..1122, aa:Gln)
FT   /note= "CDS does not include start codon"
FT   /partial
XX
PN WO200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-AU01388.
XX
PR 27-OCT-2000; 2000AU-0001078.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD;
XX
DR WPI; 2002-454646/48.
DR P-PSDB; AAE24168.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Example; Fig 4; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is human DPP9 cDNA.
XX
SQ Sequence 3024 BP; 624 A; 973 C; 875 G; 552 T; 0 other;

Alignment Scores:

Pred. No.:	2.63e-282	Length:	3024
Score:	2863.00	Matches:	516
Percent Similarity:	77.38%	Conservative:	134
Best Local Similarity:	61.43%	Mismatches:	188
Query Match:	60.91%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x AAD38954 (1-3024)

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Db    2548 CCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATGGCCTACGAC 2607

Qy     773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
           |||||||||||||||||||||||||      |||:::   |||:::   ||||||
Db    2608 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2667

Qy     793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
           ||||||||||||:::      ||||||   |||:::|||||||||||||||||:::|||
Db    2668 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2727

Qy     813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
           ||||||||||||||||||||||||||||||   ||||||:::   |||:::|||   |||
Db    2728 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2787

Qy     833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
           :::||||||||||||||||||   ||||||||||||||   ||||||||||||||||||
Db    2788 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2847

Qy     853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
           ||||||||||||||||||||||:::   |||||||||:::|||||||||   |||
Db    2848 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTACTGCACTTTCTACAGGAATACCTC 2907

RESULT 20
AAD38957
ID   AAD38957 standard; DNA; 2495 BP.
XX
AC   AAD38957;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Human dipeptidyl peptidase 4 (DPP4)-like 2 DNA.
XX
KW   Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW   autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW   graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2493
FT                   /*tag= a
FT                   /product= "Human DPP4-like 2 protein"
FT                   /transl_except= (pos: 703..705, aa:Gln)
FT                   /note= "CDS does not include start codon"
FT                   /partial
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
DR   WPI; 2002-454646/48.
DR   P-PSDB; AAE24171.
XX
PT   New dipeptidyl peptidase (DPP) peptides, useful for screening
PT   inhibitors of DPP catalytic activity, which may be employed to treat
PT   e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT   rejection and HIV infection -
XX
PS   Disclosure; Page 86-88; 91pp; English.
XX
CC   The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC   polynucleotides encoding such proteins. The DPP peptides are useful for
CC   screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC   for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC   rejection and HIV (human immuno deficiency virus) infection. The present
CC   sequence is human DPP4-like 2 DNA.
XX
SQ   Sequence 2495 BP; 535 A; 783 C; 696 G; 481 T; 0 other;

Alignment Scores:
Pred. No.:                1.44e-279      Length:          2495
Score:                    2835.00        Matches:         512
Percent Similarity:       77.47%         Conservative:    131
Best Local Similarity:    61.69%         Mismatches:      185
Query Match:              60.32%         Indels:          2
DB:                       24             Gaps:            2

US-10-070-464-1 (1-882) x AAD38957 (1-2495)

Qy      45 LeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMetAlaLysAlaPro 64
           |||:::   ::::::      :::||||||||||   |||   ::::::   |||||||||
Db       1 CTCCGGAGCATCATCCACGGCAGCCGCAAGTACTCGGGCCTCATTGTCAACAAGGCGCCC 60

Qy      65 HisAspPheMetPheValLysArgAsnAspProAspGlyProHisSerAspArgIleTyr 84
           |||||||||   ||||||::::::   |||       ||||||||||||   |||:::|||
Db      61 CACGACTTCCAGTTTGTGCAGAAGACGGATGAGTCTGGGCCCCACTCCCACCGCCTCTAC 120

Qy      85 TyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSerGluIleProLys 104
           ||||||   |||           :::||||||||||:::|||   ||||||||||||||||||
Db     121 TACCTGGGAATGCCATATGGCAGCCGGGAGAACTCCCTCCTCTACTCTGAGATTCCCAAG 180

Qy     105 ThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeuAspLeuPheGln 124
           :::   :::   |||:::|||:::||||||||||   :::||||||
Db     181 AAGGTCCGGAAAGAGGCTCTGCTGCTCCTGTCCTGGAAGCAGATGCTGGATCATTTCCAG 240

Qy     125 AlaThrLeuAspTyrGlyMetTyrSerArgGluGluGluLeuArgGluArgLysArg 144
           ||||||      :::|||:::||||||||||||||||||||||||||||||||||||||||
Db     241 GCCACGCCCCACCATGGGGTCTACTCTCGGGAGGAGGAGCTGCTGAGGGAGCGGAAACGC 300

Qy     145 IleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGlyThrPheLeuPhe 164
           :::|||      ||||||   |||||||||:::|||      ||||||   |||||||||
Db     301 CTGGGGGTCTTCGGCATCACCTCCTACGACTTCCACAGCGAGAGTGGCCTCTTCCTCTTC 360

Qy     165 GlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGlyPheThrGlnGln 184
           ||||||   :::   ::::::|||   :::||||||||||      ||||||
Db     361 CAGGCCAGCAACAGCCTCTTCCACTGCCGCGACGGCGGCAAGAACGGCTTCATGGTGTCC 420

Qy     185 ProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAspProLysLeu 204
           |||::::::|||      ::::::|||   |||          ||||||||||||||:::
Db     421 CCTATGAAACCGCTGGAAATCAAGACCCAGTGCTCAGGGCCCCGGATGGACCCCAAAATC 480

Qy     205 CysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIleTrpIleSerAsn 224
           ||||||||||||||   :::   :::|||   ::::::::::|||:::|||:::::|||
Db     481 TGCCCTGCCGACCCTGCCTTCTTCTCCTTCAACAATAACAGCGACCTGTGGGTGGCCAAC 540

Qy     225 IleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeuAlaAsnMetGlu 244
           |||   |||   ||||||||||||||||||:::   |||       |||:::|||:::
Db     541 ATCGAGACAGGCGAGGAGCGGCGGCTGACCTTCTGCCACCAAGGTTTATCCAATGTCCTG 600

Qy     245 GluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPheAspArgTyr 264
           :::|||   :::||||||||||||||||||||||||:::||||||||||||||||||:::
Db     601 GATGACCCCAAGTCTGCGGGTGTGGCCACCTTCGTCATACAGGAAGAGTTCGACCGCTTC 660

Qy     265 SerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly---LysIleLeu 283
           :::||||||||||||||||||   |||              |||   |||   |||   |||
Db     661 ACTGGGTACTGGTGGTGCCCCACAGCCTCCTGGGAAGGTTCAGAGGGCCTCAAGACGCTG 720

Qy     284 ArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisValThrSerPro 303
           ||||||||||||||||||   ||||||||||||||||:::|||||||||   ||||||
Db     721 CGAATCCTGTATGAGGAAGTCGATGAGTCCGAGGTGGAGGTCATTCACGTCCCCTCTCCT 780

Qy     304 MetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThrAlaAsnPro 323
           ||||||   |||:::   ||||||::|||||||||:::||||||:::   ||||||
Db     781 GCGCTAGAAGAAAGGAAGACGGACTCGTATCGGTACCCCAGGACAGGCAGCAAGAATCCC 840

Qy     324 LysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIleAspVal 343
           |||:::      |||:::::::|||         |||::::::|||:::|||:::
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Db    841 AAGATTGCCTTGAAACTGGCTGAGTTCCAGACTGACAGCCAGGGCAAGATCGTCTCGACC 900

Qy    344 IleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGluTyrIleAla 363

Db    901 CAGGAGAAGGAGCTGGTGCAGCCCTTCAGCTCGCTGTTCCCGAAGGTGGAGTACATCGCC 960

Qy    364 ArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAspArgSerGln 383

Db    961 AGGGCCGGGTGGACCCGGGATGGCAAATACGCCTGGGCCATGTTCCTGGACCGGCCCCAG 1020

Qy    384 ThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGluAspAspVal 403

Db   1021 CAGTGGCTCCAGCTCGTCCTCCTCCCCCCGGCCCTGTTCATCCCGAGCACAGAGAATGAG 1080

Qy    404 MetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeuIleIleTyr 423

Db   1081 GAGCAGCGGCTAGCCTCTGCCAGAGCTGTCCCCAGGAATGTCCAGCCGTATGTGGTGTAC 1140

Qy    424 GluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPheProGlnSer 443

Db   1141 GAGGAGGTCACCAACGTCTGGATCAATGTTCATGACATCTTCTATCCCTTCCCCCAATCA 1200

Qy    444 His---GluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheArgHis 462

Db   1201 GAGGGAGAGGACGAGCTCTGCTTTCTCCGCGCCAATGAATGCAAGACCGGCTTCTGCCAT 1260

Qy    463 LeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGlyGlyLeu 482

Db   1261 TTGTACAAAGTCACCGCCGTTTTAAAATCCCAGGGCTACGATTGGAGTGAGCCCTTCAGC 1320

Qy    483 ProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSerGlyGlu 502

Db   1321 CCCGGGGAAGATGAATTTAAGTGCCCCATTAAGGAAGAGATTGCTCTGACCAGCGGTGAA 1380

Qy    503 TrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArgLeuVal 522

Db   1381 TGGGAGGTTTTGGCGAGGCACGGCTCCAAGATCTGGGTCAATGAGGAGACCAAGCTGGTG 1440

Qy    523 TyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSerTyrVal 542

Db   1441 TACTTCCAGGGCACCAAGGACACGCCGCTGGAGCACCACCTCTACGTGGTCAGCTATGAG 1500

Qy    543 AsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCysIleSer 562

Db   1501 GCGGCCGGCGAGATCGTACGCCTCACCACGCCCGGCTTCTCCCATAGCTGCTCCATGAGC 1560

Qy    563 GlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCysValSer 582

Db   1561 CAGAACTTCGACATGTTCGTCAGCCACTACAGCAGCGTGAGCACGCCGCCCTGCGTGCAC 1620

Qy    583 LeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPheTrpAla 602

Db   1621 GTCTACAAGCTGAGCGGCCCCGACGACGACCCCCTGCACAAGCAGCCCCGCTTCTGGGCT 1680

Qy    603 ThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePheSerPhe 622

Db   1681 AGCATGATGGAGGCAGCCAGCTGCCCCCCGGATTATGTTCCTCCAGAGATCTTCCATTTC 1740

Qy    623 GluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeuGlnPro 642

Db   1741 CACACGCGCTCGGATGTGCGGCTCTACGGCATGATCTACAAGCCCCACGCCTTGCAGCCA 1800

Qy    643 GlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeuValAsn 662

Db   1801 GGGAAGAAGCACCCCACCGTCCTCTTTGTATATGGAGGCCCCCAGGTGCAGCTGGTGAAT 1860

Qy    663 AsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrVal 682

Db   1861 AACTCCTTCAAAGGCATCAAGTACTTGCGGCTCAACACACTGGCCTCCCTGGGCTACGCC 1920

Qy    683 ValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGlyAlaPhe 702

Db   1921 GTGGTTGTGATTGACGGCAGGGGCTCCTGTCAGCGAGGGCTTCGGTTCGAAGGGGCCCTG 1980

Qy    703 LysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyrLeuAla 722

Db   1981 AAAAACCAAATGGGCCAGGTGGAGATCGAGGACCAGGTGGAGGGCCTGCAGTTCGTGGCC 2040

Qy    723 SerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyrGlyGly 742

Db   2041 GAGAAGTATGGCTTCATCGACCTGAGCCGAGTTGCCATCCATGGCTGGTCCTACGGGGGC 2100

Qy    743 TyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIleAlaGly 762

Db   2101 TTCCTCTCGCTCATGGGGCTAATCCACAAGCCCCAGGTGTTCAAGGTGGCCATCGCGGGT 2160

Qy    763 AlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMetGlyHis 782

Db   2161 GCCCCGGTCACCGTCTGGATGGCCTACGACACAGGGTACACTGAGCGCTACATGGACGTC 2220

Qy    783 ProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGluLysPhe 802

Db   2221 CCTGAGAACAACCAGCACGGCTATGAGGCGGGTTCCGTGGCCCTGCACGTGGAGAAGCTG 2280

Qy    803 ProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnValHisPhe 822

Db   2281 CCCAATGAGCCCAACCGCTTGCTTATCCTCCACGGCTTCCTGGACGAAAACGTGCACTTT 2340

Qy    823 AlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAspLeuGln 842

Db   2341 TTCCACACAAACTTCCTCGTCTCCCAACTGATCCGAGCAGGGAAACCTTACCAGCTCCAG 2400

Qy    843 IleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyrGluLeu 862

Db   2401 ATCTACCCCAACGAGAGACACAGTATTCGCTGCCCCGAGTCGGGCGAGCACTATGAAGTC 2460

Qy    863 HisLeuLeuHisTyrLeuGlnGluAsnLeu 872

Db   2461 ACGTTACTGCACTTTCTACAGGAATACCTC 2490
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RESULT 21
AAD38955
ID   AAD38955 standard; cDNA; 3287 BP.
XX
AC   AAD38955;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Alternative version of murine dipeptidyl peptidase 9 (DPP9) cDNA.
XX
KW   Murine; dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;
KW   human immuno deficiency virus; graft rejection; cytostatic; autoimmunity;
KW   type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme; gene; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2610
FT                   /*tag= a
FT                   /product= "Murine DPP9 protein"
FT                   /note= "CDS does not include start codon"
FT                   /partial
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
```

DR WPI; 2002-454646/48.
DR P-PSDB; AAE24169.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Disclosure; Page 67-70; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is an alternative version of murine DPP9 cDNA.
CC Note: This sequence is stated to be the same as that shown as
CC SEQ ID NO: 3 in figure 9 of the specification. However these sequences
CC differ.
XX
SQ Sequence 3287 BP; 744 A; 970 C; 877 G; 696 T; 0 other;

Alignment Scores:

Pred. No.:	3.52e-279	Length:	3287
Score:	2833.00	Matches:	511
Percent Similarity:	76.79%	Conservative:	134
Best Local Similarity:	60.83%	Mismatches:	193
Query Match:	60.28%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x AAD38955 (1-3287)

```
Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||  |||:::::::::|||||      |||:::  ::::::      :::||||||
Db      88 TTCTGTGTGCAGAAGCACTCGTGGGATGGGCTGCGTAGCATTATCCACGGCAGTCGCAAG 147

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
              |||   ::::::::::||||||||||||||||||||   ||||||::::::   |||
Db     148 TCCTCGGGCCTCATTGTCAGCAAGGCCCCCCACGACTTCCAGTTTGTGCAGAAGCCTGAC 207

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
              ||||||||||||   |||:::||||||||||   |||          :::||||||
Db     208 GAGTCTGGCCCCCACTCTCACCGTCTCTATTACCTCGGAATGCCTTACGGCAGCCGTGAG 267

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||   ||||||||||||||||   :::   :::   |||:::|||:::|||
Db     268 AACTCCCTCCTCTACTCCGAGATCCCCAAGAAAGTGCGGAAGGAGGCCCTGCTGCTGCTG 327

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||   :::||||||   ||||||||||||      :::|||:::||||||||||
Db     328 TCCTGGAAGCAGATGCTGGACCACTTCCAGGCCACACCCCACCATGGTGTCTACTCCCGA 387

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||:::|||      ||||||   ||||||||||
Db     388 GAGGAGGAGCTACTGCGGGAGCGCAAGCGCCTGGGCGTCTTCGGAATCACCTCTTATGAC 447

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||   ||||||||||||||   :::   :::::::|||   :::
Db     448 TTCCACAGTGAGAGCGGCCTCTTCCTCTTCCAGGCCAGCAATAGCCTGTTCCACTGCAGG 507

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||      ||||||      |||::::::|||      ::::::|||
Db     508 GATGGTGGCAAGAATGGCTTTATGGTGTCCCCGATGAAGCCACTGGAGATCAAGACTCAG 567

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
           |||         ||||||||||||||:::||||||||||||||||   :::   ::::||
Db     568 TGTTCTGGGCCACGCATGGACCCCAAAATCTGCCCCGCAGACCCTGCCTTCTTTTCCTTC 627

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
           |||::::::::|||:::|||::::::||||||   |||   ||||||||||||||||||
Db     628 ATCAACAACAGTGATCTGTGGGTGGCAAACATCGAGACTGGGGAGGAACGGCGGCTCACC 687

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
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           :::   |||         |||   :::  ::::::   :::||||||||||||||||||
Db     688 TTCTGTCACCAGGGTTCAGCTGGTGTCCTGGACAATCCCAAATCAGCAGGCGTGGCCACC 747

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
           ||||||:::||||||||||||||||||:::::|||   ||||||||||   |||
Db     748 TTTGTCATCCAGGAGGAGTTCGACCGCTTCACTGGGTGCTGGTGGTGCCCCACGGCCTCT 807

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
                 |||   |||   |||   ||||||||||||||||||||   |||||||||
Db     808 TGGGAAGGCTCCGAAGGTCTCAAGACGCTGCGCATCCTATATGAGGAAGTGGACGAGTCT 867

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
           |||||||||:::|||||||||   ||||||   ||||||   |||:::   ||||||:::
Db     868 GAAGTGGAGGTCATTCATGTGCCCTCCCCCGCCCTGGAGGAGAGGAAGACGGACTCCTAC 927

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
           |||||||||:::|||||:::   ||||||||||:::      |||:::::::|||:::
Db     928 CGCTACCCCAGGACAGGCAGCAAGAACCCCAAGATTGCCCTGAAGCTGGCTGAGCTCCAG 987

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
              |||   :::|||:::|||:::          :::|||||||||:::|||||||||
Db     988 ACGGACCATCAGGGCAAAATCGTGTCAAGCTGCGAGAAGGAACTGGTACAGCCATTCAGC 1047

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
           ||||||      ||||||||||||||||||||||||||||||   :::|||||||||
Db    1048 TCCCTTTTCCCCAAAGTGGAGTACATCGCCCGGGCTGGCTGGACACGGGACGGCAAATAT 1107

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
           ||||||::::::   |||||||||   |||   ||||||||||:::|||||:::   |||
Db    1108 GCCTGGGCCATGTTCCTGGACCGTCCCCAGCAACGGCTTCAGCTTGTCCTCCTGCCCCCT 1167

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
              ||||||||||||      :::          :::||||||            :::|||
Db    1168 GCTCTCTTCATCCCGGCCGTTGAGAGTGAGGCCCAGCGGCAGGCAGCTGCCAGAGCCGTC 1227

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
           |||   :::|||   |||   :::||||||||||||   |||:::::|||||||:::
Db    1228 CCCAAGAATGTGCAGCCCTTTGTCATCTATGAAGAAGTCACCAATGTCTGGATCAACGTC 1287

Qy     434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
           ||||||||||||||   ||||||||:::      :::::::::      |||:::
Db    1288 CACGACATCTTCCACCCGTTTCCTCAGGCTGAGGGCCAGCAGGACTTTTGTTTCCTTCGT 1347

Qy     453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
           |||:::||||||||||||||||||   ||||||||:::::::|||      ||||||
Db    1348 GCCAACGAATGCAAGACTGGCTTCTGCCACCTGTACAGGGTCACAGTGGAACTTAAAACC 1407

Qy     473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
                 |||         |||          :::||||||||||||||
Db    1408 AAGGACTATGACTGGACGGAACCCCTCAGCCCTACAGAAGGTGAGTTTAAGTGCCCCATC 1467

Qy     493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
           |||||||||:::|||:::||||||||||||||||||||||||   ||||||||||||
Db    1468 AAGGAGGAGGTCGCCCTGACCAGTGGCGAGTGGGAGGTCTTGTCGAGGCATGGCTCCAAG 1527

Qy     513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
           |||   |||:::|||      :::||||||||||||||:::||||||||||||:::||||||
Db    1528 ATCTGGGTCAACGAGCAGACGAAGCTGGTGTACTTTCAAGGTACAAAGGACACACCGCTG 1587

Qy     533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
           ||||||||||||||||||||||||||||||   :::   |||||||:::   |||||||||
Db    1588 GAACATCACCTCTATGTGGTCAGCTACGAGTCAGCAGGCGAGATCGTGCGGCTCACCACG 1647

Qy     553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
              |||:::||||||||||   :::|||||      |||   |||:::|||   |||
Db    1648 CTCGGCTTCTCCCACAGCTGCTCCATGAGCCAGAGCTTCGACATGTTCGTGAGTCACTAC 1707

Qy     573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
           |||:::         |||   ||||||   :::||||||||||||   |||:::||||||
Db    1708 AGCAGTGTGAGCACGCCACCCTGTGTACATGTGTACAAGCTGAGCGGCCCCGATGATGAC 1767

Qy     593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
           |||      |||         |||||||||:::::::::::::::|||         |||
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Db   1768 CCACTGCACAAGCAACCACGCTTCTGGGCCAGCATGATGGAGGCAGCCAATTGCCCCCCA 1827

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db   1828 GACTATGTGCCCCCTGAGATCTTCCACTTCCACACCCGTGCAGACGTGCAGCTCTACGGC 1887

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db   1888 ATGATCTACAAGCCACACACCCTGCAACCTGGGAGGAAGCACCCCACTGTGCTCTTTGTC 1947

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db   1948 TATGGGGGCCCACAGGTGCAGTTGGTGAACAACTCCTTTAAGGGCATCAAATACCTGCGG 2007

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db   2008 CTAAATACACTGGCATCCTTGGGCTATGCTGTGGTGGTGATCGATGGTCGGGGCTCCTGT 2067

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db   2068 CAGCGGGGCCTGCACTTCGAGGGGGCCCTGAAAAATCAAATGGGCCAGGTGGAGATTGAG 2127

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db   2128 GACCAGGTGGAAGGCTTGCAGTACGTGGCTGAGAAGTATGGCTTCATTGACTTGAGCCGA 2187

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db   2188 GTCGCCATCCATGGCTGGTCCTACGGCGGCTTCCTCTCACTCATGGGGCTCATCCACAAG 2247

Qy    753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
Db   2248 CCACAAGTGTTCAAGGTAGCCATTGCGGGCGCTCCTGTCACTGTGTGGATGGCCTATGAC 2307

Qy    773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
Db   2308 ACAGGGTACACGGAACGATACATGGATGTCCCCGAAAATAACCAGCAAGGCTATGAGGCA 2367

Qy    793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
Db   2368 GGGTCTGTAGCCCTGCATGTGGAGAAGCTGCCCAATGAGCCTAACCGCCTGCTTATCCTC 2427

Qy    813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db   2428 CACGGCTTCCTGGACGAGAACGTTCACTTCTTCCACACAAATTTCCTGGTGTCCCAGCTG 2487

Qy    833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
Db   2488 ATCCGAGCAGGAAAGCCATACCAGCTTCAGATCTACCCAAACGAGAGACATAGCATCCGC 2547

Qy    853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
Db   2548 TGCCGCGAGTCCGGAGAGCATTACGAGGTGACGCTGCTGCACTTTCTGCAGGAACACCTG 2607
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RESULT 22
ABK83339
ID ABK83339 standard; cDNA; 4180 BP.
XX
AC ABK83339;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-2 splice variant #7:
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61608.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 97-98; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4180 BP; 898 A; 1312 C; 1178 G; 792 T; 0 other;

Alignment Scores:

Pred. No.:	9.67e-278	Length:	4180
Score:	2820.50	Matches:	510
Percent Similarity:	76.43%	Conservative:	132
Best Local Similarity:	60.71%	Mismatches:	183
Query Match:	60.01%	Indels:	15
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x ABK83339 (1-4180)

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Qy     35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
Db    436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy     55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
Db    496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy     75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
Db    556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy     95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
Db    616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy    115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
Db    676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy    135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
Db    736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795
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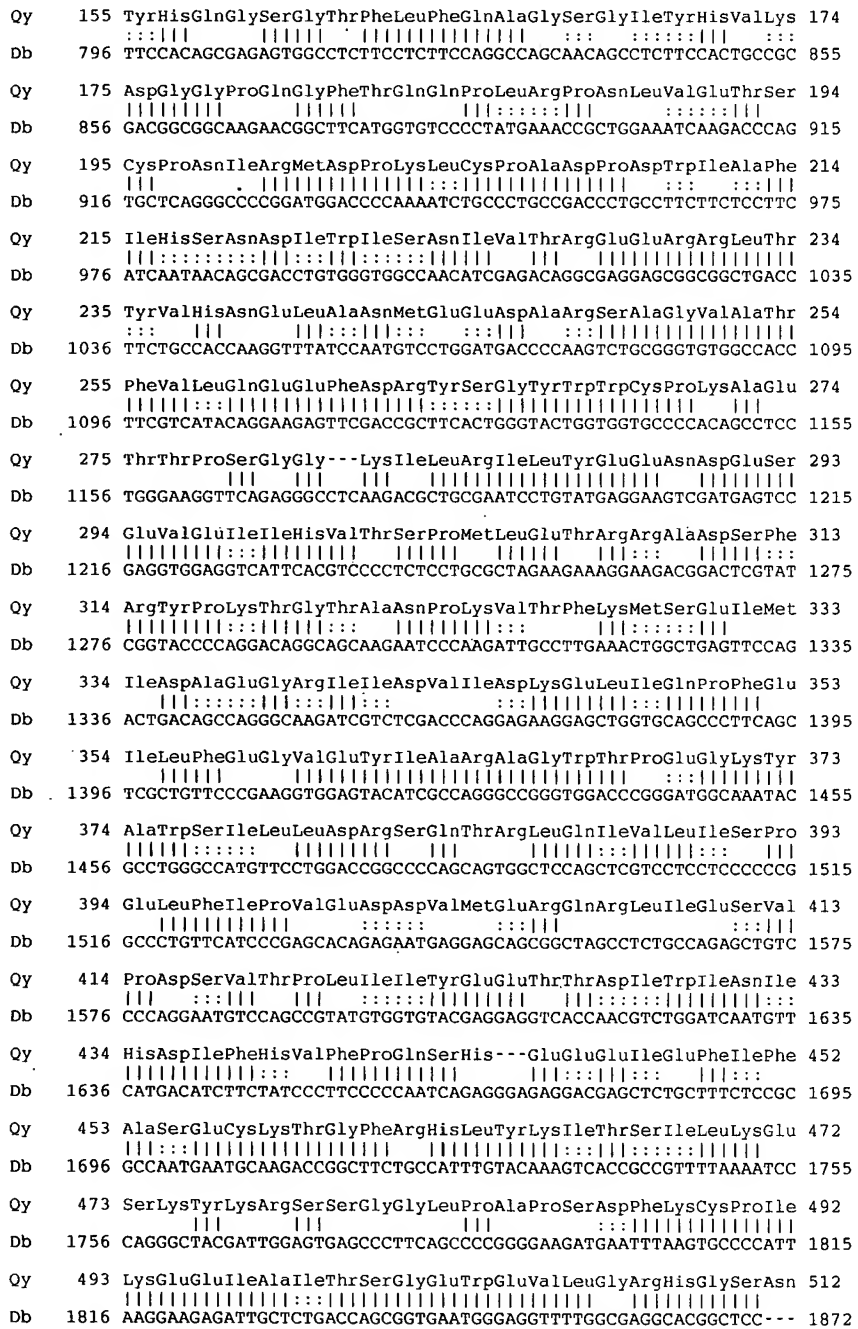
Qy 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
Db 796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855
Qy 175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
Db 856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915
Qy 195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
Db 916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975
Qy 215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
Db 976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035
Qy 235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
Db 1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095
Qy 255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
Db 1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155
Qy 275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
Db 1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215
Qy 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
Db 1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275
Qy 314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
Db 1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335
Qy 334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
Db 1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395
Qy 354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
Db 1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455
Qy 374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
Db 1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515
Qy 394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
Db 1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575
Qy 414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
Db 1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635
Qy 434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPhePhePhe 452
Db 1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695
Qy 453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db 1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755
Qy 473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db 1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815
Qy 493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db 1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCC--- 1872
Qy 513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db 1873 ----------AAGGGCACCAAGGACACGCCGCTG 1896
Qy 533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db 1897 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1956
Qy 553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db 1957 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2016
Qy 573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db 2017 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2076
Qy 593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db 2077 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2136
Qy 613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db 2137 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2196
Qy 633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db 2197 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2256
Qy 653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db 2257 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2316
Qy 673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db 2317 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2376
Qy 693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db 2377 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2436
Qy 713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db 2437 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2496
Qy 733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db 2497 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2556
Qy 753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
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Qy 773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
Db 2617 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2676
Qy 793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
Db 2677 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2736
Qy 813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db 2737 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2796
Qy 833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
Db 2797 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2856
Qy 853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
Db 2857 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2916

RESULT 23

ABK83338
ID ABK83338 standard; cDNA; 4263 BP.
XX
AC ABK83338;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-2 splice variant #6.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61607.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
XX
PS Disclosure; Page 93-94; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4263 BP; 913 A; 1342 C; 1209 G; 799 T; 0 other;

Alignment Scores:

Pred. No.:	9.97e-278	Length:	4263
Score:	2820.50	Matches:	510
Percent Similarity:	76.43%	Conservative:	132
Best Local Similarity:	60.71%	Mismatches:	183
Query Match:	60.01%	Indels:	15
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x ABK83338 (1-4263)

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Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||  |||:::::::::||||||     |||:::  ::::::     :::||||||
Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||  :::|||  |||  ::::::||||||||||  |||::::::||||||||||:::
Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           ||||||||||||  |||:::|||||||||  |||  :::  :::||||||||
Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||  ||||||||||||||||  :::  :::  |||:::|||:::|||
Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||  :::|||||||  ||||||||||||  :::|||:::|||||||||
Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||:::|||  ||||||  |||||||||
Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||  ||||||  ||||||||||||||  :::  :::::::|||  :::
Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||  ||||||  |||:::::::|||  :::::::|||
Db     856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
           |||  ||||||||||||||:::|||||||||||||||  :::  :::|||
Db     916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
           .  |||:::::::|||:::|||:::::|||||  |||  ||||||||||||||||||
Db     976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
           :::  |||  |||:::|||:::  :::|||  :::||||||||||||||||||
Db    1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
           ||||||:::||||||||||||||||:::::||||||||||||||||  |||
Db    1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
                |||  |||  |||  ||||||||||||||||||||  |||||||||
Db    1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
           ||||||||||:::|||||||||  ||||||  ||||||  |||:::  |||||||::
Db    1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
           |||||||||:::|||||:::  ||||||||:::  |||:::::|||
Db    1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
           |||:::::::|||:::|||:::         :::|||||||||:::|||||||||
Db    1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
           ||||||  ||||||||||||||||||||||||||||||  :::|||||||||
Db    1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
           ||||||::::::  |||||||||  |||  ||||||:::|||||||:::  |||
Db    1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
           ||||||||||||  ::::::  :::|||  :::|||
Db    1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
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Db   1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy    434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755

Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCC--- 1872

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db   1873 ----------------------------------AAGGGCACCAAGGACACGCCGCTG 1896

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db   1897 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1956

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db   1957 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2016

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db   2017 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2076

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db   2077 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2136

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db   2137 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2196

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db   2197 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2256

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db   2257 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2316

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db   2317 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2376

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db   2377 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2436

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db   2437 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2496

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db   2497 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2556

Qy    753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
Db   2557 CCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATGGCCTACGAC 2616

Qy    773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
Db   2617 ACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGCTATGAGGCG 2676

Qy    793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
Db   2677 GGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTGCTTATCCTC 2736

Qy    813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db   2737 CACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACTG 2796

Qy    833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg 852
Db   2797 ATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCGC 2856

Qy    853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
Db   2857 TGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2916
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RESULT 24
AAD38311
ID AAD38311 standard; cDNA; 2751 BP.
XX
AC AAD38311;
XX
DT 23-SEP-2002 (first entry)
XX
DE Murine dipeptidyl peptidase 9 (DPP9) cDNA.
XX
KW Murine; dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;
KW human immuno deficiency virus; graft rejection; cytostatic; autoimmunity;
KW type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme; gene; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 2..2545
FT /*tag= a
FT /product= "Murine DPP9 protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN WO200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-AU01388.
XX
PR 27-OCT-2000; 2000AU-0001078.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD;
XX
DR WPI; 2002-454646/48.
DR P-PSDB; AAE23875.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Disclosure; Fig 9; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is an alternative version of murine DPP9 cDNA.
CC Note: This sequence is stated to be the same as that shown as
CC SEQ ID NO: 3 in the sequence listing of the specification. However these
CC sequences differ.
XX

SQ Sequence 2751 BP; 615 A; 820 C; 761 G; 555 T; 0 other;

Alignment Scores:

Pred. No.:	3.92e-272	Length:	2751
Score:	2763.00	Matches:	508
Percent Similarity:	72.18%	Conservative:	133
Best Local Similarity:	57.21%	Mismatches:	194
Query Match:	58.79%	Indels:	54
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x AAD38311 (1-2751)

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Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
Db      89 TTCTGTGTGCAGAAGCACTCGTGGGATGGGCTGCGTAGCATTATCCACGGCAGTCGCAAG 148

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
Db     149 TCCTCGGGCCTCATTGTCAGCAAGGCCCCCCACGACTTCCAGTTTGTGCAGAAGCCTGAC 208

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
Db     209 GAGTCTGGCCCCCACTCTCACCGTCTCTATTACCTCGGAATGCCTTACGGCAGCCGTGAG 268

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
Db     269 AACTCCCTCCTCTACTCCGAGATCCCCAAGAAAGTGCGGAAGGAGGCCCTGCTGCTGCTG 328

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
Db     329 TCCTGGAAGCAGATGCTGGACCACTTCCAGGCCACACCCCACCATGGTGTCTACTCCCGA 388

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
Db     389 GAGGAGGAGCTACTGCGGGAGCGCAAGCGCCTGGGCGTCTTCGGAATCACCTCTTATGAC 448

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
Db     449 TTCCACAGTGAGAGCGGCCTCTTCCTCTTCCAGGCCAGCAATAGCCTGTTCCACTGCAGG 508

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
Db     509 GATGGTGGCAAGAATGGCTTTATGGTGTCCCCGATGAAGCCACTGGAGATCAAGACTCAG 568

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
Db     569 TGTTCTGGGCCACGCATGGACCCCAAAATCTGCCCCGCAGACCCTGCCTTCTTTTCCTTC 628

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
Db     629 ATCAACAACAGTGATCTGTGGGTGGCAAACATCGAGACTGGGGAGGAACGGCGGCTCACC 688

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
Db     689 TTCTGTCACCAGGGTTCAGCTGGTGTCCTGGACAATCCCAAATCAGCAGGCGTGGCCACC 748

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
Db     749 TTTGTCATCCAGGAGGAGTTCGACCGCTTCACTGGGTGCTGGTGGTGCCCCACGGCCTCT 808

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
Db     809 TGGGAAGGCTCCGAAGGTCTCAAGACGCTGCGCATCCTATATGAGGAAGTGGACGAGTCT 868

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
Db     869 GAAGTGGAGGTCATTCATGTGCCCTCCCCCGCCCTGGAGGAGAGGAAGACGGACTCCTAC 928

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
Db     929 CGCTACCCCAGGACAGGCAGCAAGAACCCCAAGATTGCCCTGAAGCTGGCTGAGCTCCAG 988

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
Db     989 ACGGACCATCAGGGCAAAATCGTGTCAAGCTGCGAGAAGGAACTGGTACAGCCATTCAGC 1048

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
Db    1049 TCCCTTTTCCCCAAAGTGGAGTACATCGCCCGGGCTGGCTGGACACGGGACGGCAAATAT 1108

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
Db    1109 GCCTGGGCCATGTTCCTGGACCGTCCCCAGCAACGGCTTCAGCTTGTCCTCCTGCCCCCT 1168

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
Db    1169 GCTCTCTTCATCCCGGCCGTTGAGAGTGAGGCCCAGCGGCAGGCAGCTGCCAGAGCCGTC 1228

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
Db    1229 CCCAAGAATGTGCAGCCCTTTGTCATCTATGAAGAAGTCACCAATGTCTGGATCAACGTC 1288

Qy     434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
Db    1289 CACGACATCTTCCACCCGTTTCCTCAGGCTGAGGGCCAGCAGGACTTTTGTTTCCTTCGT 1348

Qy     453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db    1349 GCCAACGAATGCAAGACTGGCTTCTGCCACCTGTACAGGGTCACAGTGGAACTTAAAACC 1408

Qy     473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db    1409 AAGGACTATGACTGGACGGAACCCCTCAGCCCTACAGAAGGTGAGTTTAAGTGCCCCATC 1468

Qy     493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db    1469 AAGGAGGAGGTCGCCCTGACCAGTGGCGAGTGGGAGGTCTTGTCGAGGCATGGCTCCAAG 1528

Qy     513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db    1529 ATCTGGGTCAACGAGCAGACGAAGCTGGTGTACTTTCAAGGTACAAAGGACACACCGCTG 1588

Qy     533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db    1589 GAACATCACCTCTATGTGGTCAGCTACGAGTCAGCAGGCGAGATCGTGCGGCTCACCACG 1648

Qy     553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db    1649 CTCGGCTTCTCCCACAGCTGCTCCATGAGCCAGAGCTTCGACATGTTCGTGAGTCACTAC 1708

Qy     573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db    1709 AGCAGTGTGAGCACGCCACCCTGTGTACATGTGTACAAGCTGAGCGGCCCCGATGATGAC 1768

Qy     593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db    1769 CCACTGCACAAGCAACCACGCTTCTGGGCCAGCATGATGGAGGCAGCCAATTGCCCCCCA 1828

Qy     613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db    1829 GACTATGTGCCCCCTGAGATCTTCCACTTCCACACCCGTGCAGACGTGCAGCTCTACGGC 1888

Qy     633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db    1889 ATGATCTACAAGCCACACACCCTGCAACCTGGGAGGAAGCACCCCACTGTGCTCTTTGTC 1948

Qy     653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db    1949 TATGGGGGCCCACAGGTGCAGTTGGTGAACAACTCCTTTAAGGGCATCAAATACCTGCGG 2008

Qy     673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db    2009 CTAAATACACTGGCATCCTTGGGCTATGCTGTGGTGGTGATCGATGGTCGGGGCTCCTGT 2068

Qy     693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
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Db    2069 CAGCGGGGCCTGCACTTCGAGGGGGCCCTGAAAAATCAAATGGGCCAGGTGGAGATTGAG 2128

Qy     713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
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Db    2129 GACCAGGTGGAAGGCTTGCAGTACGTGGCTGAGAAGTATGGCTTCATTGACTTGAGCCGA 2188

Qy     733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
           |||   ||||||||||||||||||||||:::||||||||||||   |||:::   :::
Db    2189 GTCGCCATCCATGGCTGGTCCTACGGCGGCTTCCTCTCACTCATGGGGCTCATCCACAAG 2248

Qy     753 SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp 772
           :::|||:::|||||||||||||||||||||||||||:::|||:::   ||||||
Db    2249 CCACAAGTGTTCAAGGTAGCCATTGCGGGCGCTCCTGTCACTGTGTGGATGGCCTATGAC 2308

Qy     773 ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLeu 792
           ||||||||||||||||||||||      |||:::   |||:::|||||||||
Db    2309 ACAGGGTACACGGAACGATACATGGATGTCCCCGAAAATAACCAGCAAGGCTATGAGGCA 2368

Qy     793 GlySerValAlaMetGlnAlaGluLysProSerGluProAsnArgLeuLeuLeuLeu 812
           ||||||||||:::      ||||||   |||:::||||||||||||||||||:::|||
Db    2369 GGGTCTGTAGCCCTGCATGTGGAGAAGCTGCCCAATGAGCCTAACCGCCTGCTTATCCTC 2428

Qy     813 HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
           ||||||||||||||||||||||||||||||   ||||||:::   |||:::|||   |||
Db    2429 CACGGCTTCCTGGACGAGAACGTTCACTTCTTCCACACAAATTTCCTGGTGTCCCAGCTG 2488

Qy     833 ValArgAlaGlyLysProTyrAspLeuGlnIle---------------------------- 843
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Db    2489 ATCCGAGCAGGAAAGCCATACCAGCTTCAGGT-TGCATCAGTGACAACACCTCAGTGACT 2547

Qy     843 ------------------------------------------------------------ 843

Db    2548 ACCCCTCACTAAGACCCCAGTTTTGATGAACCCACTTGGCTACAGGCATGGGAGTGCCCC 2607

Qy     843 ------------------------------------------------------------ 843

Db    2608 CCAATGATTAGAGACCCAAGAGCAGTTGCCTGAGGGAGAGGACATTTAAAGGTCCAGGAC 2667

Qy     844 ------TyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyrGlu 861
                ||||||   ||||||||||||||||||      ||||||||||||||||||||
Db    2668 TGAATCTACCCAAACGAGAGACATAGCATCCGCTGCCGCGAGTCCGGAGAGCATTACGAG 2727

Qy     862 LeuHisLeuLeuHisTyrLeuGln 869
           :::   ||||||||||:::||||||
Db    2728 GTGACGCTGCTGCACTTTCTGCAG 2751

RESULT 25
ABK83337
ID   ABK83337 standard; cDNA; 4076 BP.
XX
AC   ABK83337;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-2 splice variant #5.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61606.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 90-91; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4076 BP; 879 A; 1276 C; 1143 G; 778 T; 0 other;

Alignment Scores:
Pred. No.:                3.36e-260      Length:          4076
Score:                    2649.00        Matches:         486
Percent Similarity:       72.89%         Conservative:    127
Best Local Similarity:    57.79%         Mismatches:      177
Query Match:              56.36%         Indels:          51
DB:                       24             Gaps:            3

US-10-070-464-1 (1-882) x ABK83337 (1-4076)

Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||   |||:::::::::||||||      |||:::   ::::::      :::||||||
Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||   |||   ::::::   ||||||||||||||||||   ||||||::::::   |||
Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           |||||||||||||  |||:::||||||||   |||         :::||||||
Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||  ||||||||||||||||||  :::  :::   |||:::|||:::|||
Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||   :::||||||   ||||||||||||       :::|||:::|||||||||
Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||:::|||      ||||||   ||||||||||
Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||   ||||||||||||||   :::   :::::|||   :::
Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||     ||||||         |||:::::|||      :::::|||
Db     856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915
```

```
Qy    195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
Db    916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy    215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
Db    976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy    235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
Db   1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy    255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
Db   1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy    275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
Db   1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy    294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
Db   1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy    314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
Db   1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy    334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
Db   1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy    354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
Db   1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy    374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
Db   1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy    394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
Db   1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy    414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
Db   1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy    434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755

Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCCAAG 1875

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
Db   1876 ATCTGGGTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGACACGCCGCTG 1935

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
Db   1936 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1995

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572
Db   1996 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2055

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
Db   2056 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2115

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
Db   2116 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2175

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db   2176 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2235

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db   2236 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2295

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db   2296 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2355

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db   2356 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2415

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db   2416 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2475

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db   2476 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2535

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db   2536 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2595

Qy    753 SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAs 772
Db   2596 CCCCAGGTGTTCAAGG---------------------------------------------- 2611

Qy    772 pThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLe 792
Db   2611 ---------------------------------------------------------- 2611

Qy    792 uGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuLe 812
Db   2612 ----------------------------------------CCCAACCGCTTGCTTATCCT 2631

Qy    812 uHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe 832
Db   2632 CCACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACT 2691

Qy    832 uValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleAr 852
Db   2692 GATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCG 2751

Qy    852 gValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLe 872
Db   2752 CTGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCT 2811

Qy    872 u 872
Db   2812 C 2812
```

RESULT 26
ABK83336
ID ABK83336 standard; cDNA; 4159 BP.
XX
AC ABK83336;

XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-2 splice variant #4.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR P-PSDB; ABG61605.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 87-88; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4159 BP; 894 A; 1306 C; 1174 G; 785 T; 0 other;

Alignment Scores:

Pred. No.:	3.46e-260	Length:	4159
Score:	2649.00	Matches:	486
Percent Similarity:	72.89%	Conservative:	127
Best Local Similarity:	57.79%	Mismatches:	177
Query Match:	56.36%	Indels:	51
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x ABK83336 (1-4159)

```
Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||   |||:::::::::||||||      |||:::   ::::::      :::||||||
Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||   |||   ::::::   ||||||||||||||||||   ||||||::::::   |||
Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           |||||||||||   |||:::|||||||||   |||         :::||||||
Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||   |||||||||||||||||   :::   :::   |||:::|||:::|||
Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||   :::||||||   ||||||||||||      :::|||:::|||||||||
Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||:::|||      ||||||   |||||||||
Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||   ||||||||||||||   :::   :::::::|||   :::
Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||      ||||||         |||::::::|||      ::::::|||
Db     856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
           |||         |||||||||||||||:::|||||||||||||||   :::   :::|||
Db     916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
           |||:::::::::|||:::|||:::::::||||||   |||   ||||||||||||||||||
Db     976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
           :::   |||      |||:::|||:::   :::|||   :::||||||||||||||||||
Db    1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
           ||||||:::||||||||||||||||||:::::||||||||||||||||||   |||
Db    1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
                  |||   |||   ||||||||||||||||||||   |||||||||
Db    1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
           |||||||||:::|||||||||   ||||||   ||||||   |||:::   ||||||:::
Db    1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
           |||||||||:::||||||:::   |||||||||:::      |||:::::::|||
Db    1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
              |||:::::|||:::|||:::         :::||||||||||:::||||||||||
Db    1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
              ||||||      ||||||||||||||||||||||||||||||   :::||||||||||
Db    1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
           ||||||::::::   |||||||||   |||      ||||||:::||||||:::   |||
Db    1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
              ||||||||||      ::::::      :::|||                :::|||
Db    1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
           |||   :::|||   |||   ::::::||||||||   |||::::::||||||||:::
Db    1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy     434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
           ||||||||||||:::   ||||||||||||      |||:::|||:::   |||:::
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Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
          |||:::|||||||||||||||||   ||||||||||||:::|||::::::||||||
Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755

Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
            |||      |||         |||         :::||||||||||||||||
Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512
          |||||||||||||||:::|||||||||||||||||||||||||   ||||||||||||
Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCCAAG 1875

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
          |||   |||:::|||      :::||||||||||||:::||||||||||||:::||||||
Db   1876 ATCTGGGTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGACACGCCGCTG 1935

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
          |||||||||||||||||||||||||||         |||||||:::   |||||||||
Db   1936 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1995

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPheIleSerLysTyr 572
             |||:::||||||||||||||   :::||||||:::   |||   |||:::|||   |||
Db   1996 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2055

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592
          |||:::         |||   ||||||   :::||||||||||||   |||:::|||||||
Db   2056 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2115

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612
          |||      |||         |||||||||:::::::::::::::|||         |||
Db   2116 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2175

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
          ||||||   ||||||||||||||||   |||   :::   :::         |||||||||
Db   2176 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2235

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
          |||:::||||||||||||   ||||||||||||||||||:::|||||||||||||||:::
Db   2236 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2295

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
          |||||||||||||||||||||||||||||||   |||||||||:::|||||   |||
Db   2296 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2355

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
          |||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db   2356 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2415

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
             |||||||||:::||||||||||||   |||   :::||||||||||:::||||||:::
Db   2416 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2475

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
          |||||||||||||||||||||:::::::|||   :::|||   ||||||||||||   |||
Db   2476 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2535

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
          |||   |||||||||||||||||||||||:::||||||||||||   |||:::   :::
Db   2536 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2595

Qy    753 SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAs 772
             :::||| |||
Db   2596 CCCCAGGTGTTCAAGG---------------------------------------------- 2611

Qy    772 pThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLe 792

Db   2611 ----------------------------------------:---------------------- 2611

Qy    792 uGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuLe 812
                                                  |||||||||:|||||:::||
Db   2612 ----------------------------------------CCCAACCGCTTGCTTATCCT 2631

Qy    812 uHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe 832
          |||||||||||||||||||||||||||||||   ||||||:::   |||:::|||   ||
Db   2632 CCACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACT 2691

Qy    832 uValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleAr 852
          |:::|||||||||||||||||   ||||||||||||||   ||||||||||||||||||
Db   2692 GATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCG 2751

Qy    852 gValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLe 872
          |   |||||||||||||||||||||||:::   |||||||||:::||||||||||   ||
Db   2752 CTGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCT 2811

Qy    872 u 872
          |
Db   2812 C 2812
```

RESULT 27
AAI57896
ID AAI57896 standard; cDNA; 2801 BP.
XX
AC AAI57896;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 99.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM38740.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 99; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2801 BP; 586 A; 889 C; 801 G; 525 T; 0 other;

Alignment Scores:

Pred. No.:	2.52e-259	Length:	2801
Score:	2638.00	Matches:	491
Percent Similarity:	73.16%	Conservative:	136
Best Local Similarity:	57.29%	Mismatches:	183
Query Match:	56.13%	Indels:	47
DB:	22	Gaps:	7

US-10-070-464-1 (1-882) x AAI57896 (1-2801)

```
Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||  |||:::::::::|||||      |||:::   ::::::      :::|||||||
Db     314 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 373

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||   |||   ::::::   ||||||||||||||||||   ||||||::::::   |||
Db     374 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 433

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           |||||||||||   |||:::|||||||   |||         :::||||||
Db     434 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGTATGCCATATGGCAGCCGAGAG 493

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||   ||||||||||||||||||   :::   :::   |||:::|||:::|||
Db     494 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 553

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||   :::|||||||   ||||||||||||      :::|||:::|||||||||
Db     554 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 613

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||:::|||      ||||||   |||||||||
Db     614 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 673

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||   ||||||||||||||   :::   :::::|||   :::
Db     674 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 733

Qy     175 AspGlyGlyProGlnGlyPhe--------------------ThrGlnGlnProLeuArg 187
           |||||||||      ||||||                                |||::::::
Db     734 GACGGCGGCAAGAACGGCTTCATGGTGAGCCCTGGCCCTGGCTGTGTGTCCCCTATGAAA 793

Qy     188 ProAsnLeuValGluThrSerCysProAsnIleArgMetAspProLysLeuCysProAla 207
           |||      ::::::|||   |||         ||||||||||||||::::||||||||
Db     794 CCGCTGGAAATCAAGACCCAGTGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCC 853

Qy     208 AspProAspTrpIleAlaPheIleHisSerAsnAspIleTrpIleSerAsnIleValThr 227
           ||||||   :::   :::||||||:::::::::|||:::|||:::::::||||||   |||
Db     854 GACCCTGCCTTCTTCTCCTTCATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACA 913

Qy     228 ArgGluGluArgArgLeuThrTyrValHisAsnGluLeuAlaAsnMetGluGluAspAla 247
           ||||||||||||||||||:::   |||      |||:::|||:::   :::|||
Db     914 GGCGAGGAGCGGCGGCTGACCTTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCC 973

Qy     248 ArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPheAspArgTyrSerGlyTyr 267
           :::||||||||||||||||||||||:::|||||||||||||||||||:::::||||||
Db     974 AAGTCTGCGGGTGTGGCCACCTTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTAC 1033

Qy     268 TrpTrpCysProLysAlaGluThrThrProSerGlyGly---LysIleLeuArgIleLeu 286
           ||||||||||   |||         |||   |||   |||   ||||||||||||
Db    1034 TGGTGGTGCCCCACAGCCTCCTGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTG 1093

Qy     287 TyrGluGluAsnAspGluSerGluValGluIleIleHisValThrSerProMetLeuGlu 306
           |||||||||   |||||||||||||||||||:::|||||||||   ||||||   ||||||
Db    1094 TATGAGGAAGTCGATGAGTCCGAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAA 1153

Qy     307 ThrArgArgAlaAspSerPheArgTyrProLysThrGlyThrAlaAsnProLysValThr 326
           |||:::   |||||:::|||||||||:::|||||||:::   |||||||||:::
Db    1154 GAAAGGAAGACGGACTCGTATCGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCC 1213

Qy     327 PheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIleAspValIleAspLys 346
           |||:::::::|||         |||::::::|||:::|||:::         :::|||
Db    1214 TTGAAACTGGCTGAGTTCCAGACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAG 1273

Qy     347 GluLeuIleGlnProPheGluIleLeuPheGluGlyValGluTyrIleAlaArgAlaGly 366
           ||||||:::|||||||||      ||||||      ||||||||||||||||||||||||
Db    1274 GAGCTGGTGCAGCCCTTCAGCTCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGG 1333

Qy     367 TrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeu 386
           ||||||   :::|||||||||||||||||:::::   |||||||||   |||      |||
Db    1334 TGGACCCGGGATGGCAAATACGCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTC 1393

Qy     387 GlnIleValLeuIleSerProGluLeuPheIleProValGluAspAspValMetGluArg 406
           |||:::|||||:::   |||   ||||||||||||      ::::::      :::
Db    1394 CAGCTCGTCCTCCTCCCCCCGGCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGGCG 1453

Qy     407 GlnArgLeuIleGluSer-ValProAspSerValThrProLeuIleIleTyrGluGluTh 426
           |||   :::|||  ||||||   :::|||   |||   :::      ||||||
Db    1454 GCTAGCCTCTGCCAGAGCTGTCCCCAGGAATGTCCAGCCGTATGTGTGTACGGAGGAGGT 1513

Qy     426 rThrAspIleTrpIleAsnIleHisAspIlePheHisValPheProGlnSerHis---Gl 445
           |||:::::::|||||||||:::|||||||||||:::   ||||||||||||      ||
Db    1514 CACCAACGTCTGGATCAATGTTCATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGA 1573

Qy     445 uGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheArgHisLeuTyrLy 465
           |:::|||:::   |||:::   |||:::|||||||||||||||||   ||||||||||
Db    1574 GGACGAGCTCTGCTTTCTCCGCGCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAA 1633

Qy     465 sIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGlyGlyLeuProAlaPr 485
           |:::|||:::::|||||         |||      |||      |||
Db    1634 AGTCACCGCCGTTTTAAAATCCCAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGG-- 1691

Qy     485 oSerAspPheLysCysProIleLysGluGluIleAlaIleThrSerGlyGluTrpGluVa 505
                                 :::   |||   :::::::|||:::      |||
Db    1692 ----------------------GAAGGTGAGCAGAGCCTGACGAATGCTATCTGG----- 1724

Qy     505 lLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArgLeuValTyrPheGl 525
                                        |||:::|||      :::||||||||||::
Db    1725 --------------------------GTCAATGAGGAGACCAAGCTGGTGTACTTCCA 1756

Qy     525 uGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSerTyrValAsnProGl 545
           :||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db    1757 GGGCACCAAGGACACGCCGCTGGAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGG 1816

Qy     545 yGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCysIleSerGlnHisCy 565
           ||||:::   |||||||||      |||:::||||||||||||   :::||||||:::
Db    1817 CGAGATCGTACGCCTCACCACGCCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTT 1876

Qy     565 sAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLy 585
           |||   |||:::|||   ||||||:::         |||   ||||||   :::|||||
Db    1877 CGACATGTTCGTCAGCCACTACAGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAA 1936

Qy     585 sLeuSerSerProGluAspAspProThrCysLysThrLysGluPheTrpAlaThrIleLe 605
           |||||||   |||:::|||||||||      |||         |||||||||::::::::
Db    1937 GCTGAGCGGCCCCGACGACGACCCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGAT 1996

Qy     605 uAspSerAlaGlyProLeuProAspTyrThrProProGluIlePheSerPheGluSerTh 625
           :::::::|||                              :::||||||   |||   :::
Db    1997 GGAGGCAGCC--------------------------AAGATCTTCCATTTCCACACGCG 2029

Qy     625 rThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeuGlnProGlyLysLy 645
           :::         ||||||||||||:::||||||||||||   ||||||||||||||||
Db    2030 CTCGGATGTGCGGCTCTACGGCATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAA 2089

Qy     645 sTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeuValAsnAsnArgPh 665
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```
Db    2090 GCACCCCACCGTCCTCTTTGTATATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTT 2149

Qy     665 eLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrValValValVa 685

Db    2150 CAAAGGCATCAAGTACTTGCGGCTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGT 2209

Qy     685 lIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGlyAlaPheLysTyrLy 705

Db    2210 GATTGACGGCAGGGGCTCCTGTCAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCA 2269

Qy     705 sMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTy 725

Db    2270 AATGGGCCAGGTGGAGATCGAGGACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTA 2329

Qy     725 rAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSe 745

Db    2330 TGGCTTCATCGACCTGAGCCGAGTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTC 2389

Qy     745 rLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProVa 765

Db    2390 GCTCATGGGGCTAATCCACAAGCCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGT 2449

Qy     765 lThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMetGlyHisProAspGl 785

Db    2450 CACCGTCTGGATGGCCTACGACACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAA 2509

Qy     785 nAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGluLysProSerGl 805

Db    2510 CAACCAGCACGGCTATGAGGCGGGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGA 2569

Qy     805 uProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnValHisPheAlaHisTh 825

Db    2570 GCCCAACCGCTTGCTTATCCTCCACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACAC 2629

Qy     825 rSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAspLeu---------- 841

Db    2630 AAACTTCCTCGTCTCCCAACTGATCCGAGCAGGGAAACCTTACCAGCTCCAGGTGGCCCT 2689

Qy     842 ----------------GlnIleTyrProGlnGluArgHisSerIleArgValProGluSe 856

Db    2690 GCCTCCTGTCTCCCCGCAGATCTACCCCAACGAGAGACACAGTATTCGCTGCCCCGAGTC 2749

Qy     856 rGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872

Db    2750 GGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2798

RESULT 28
ABK83341
ID   ABK83341 standard; cDNA; 4037 BP.
XX
AC   ABK83341;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-2 splice variant #9.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61610.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 103-104; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4037 BP; 869 A; 1268 C; 1131 G; 769 T; 0 other;

Alignment Scores:
Pred. No.:              3.86e-255       Length:         4037
Score:                  2599.50         Matches:        479
Percent Similarity:     71.82%          Conservative:   125
Best Local Similarity:  56.96%          Mismatches:     173
Query Match:            55.31%          Indels:         64
DB:                     24              Gaps:           4

US-10-070-464-1 (1-882) x ABK83341 (1-4037)

Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54

Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74

Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94

Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114

Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134

Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154

Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174

Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
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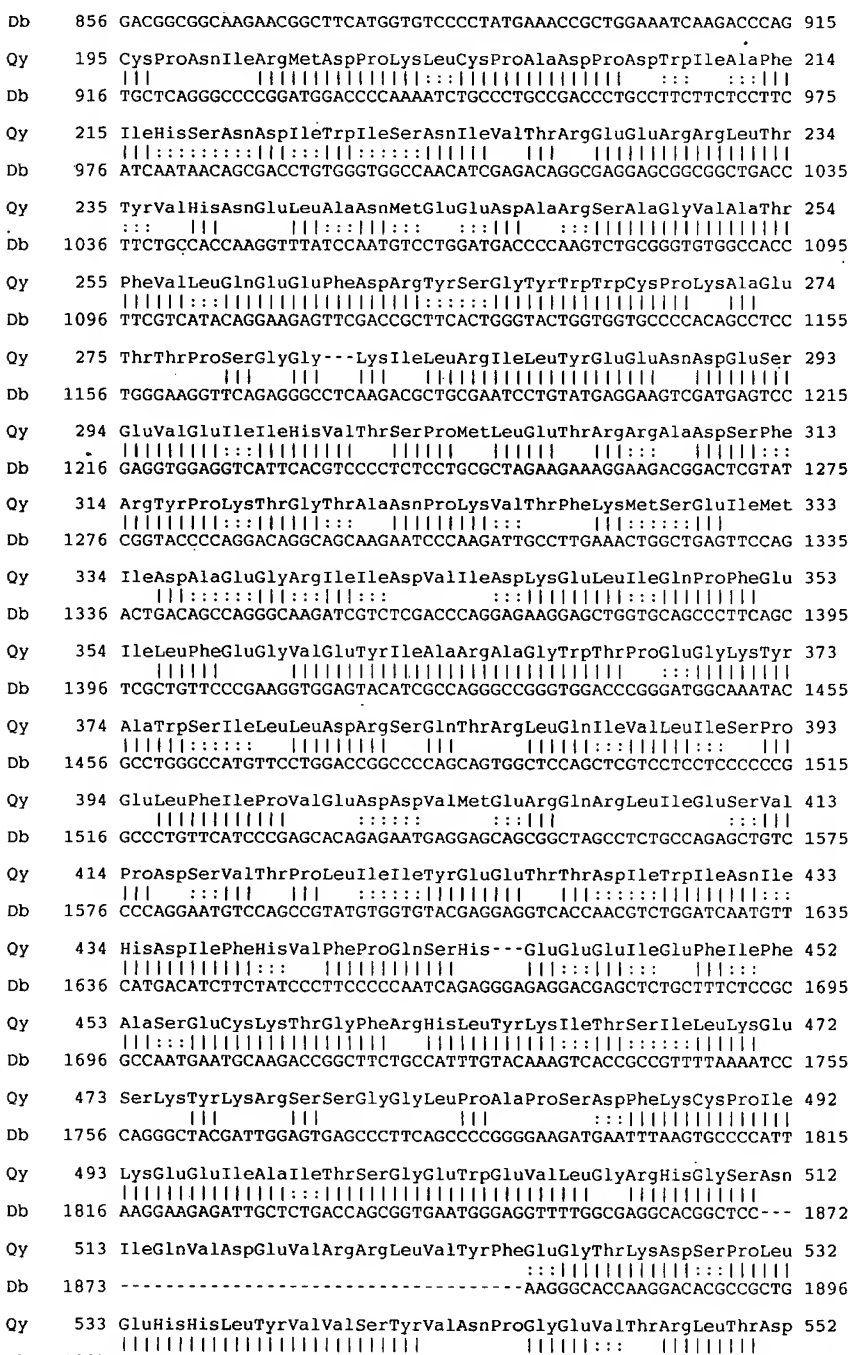

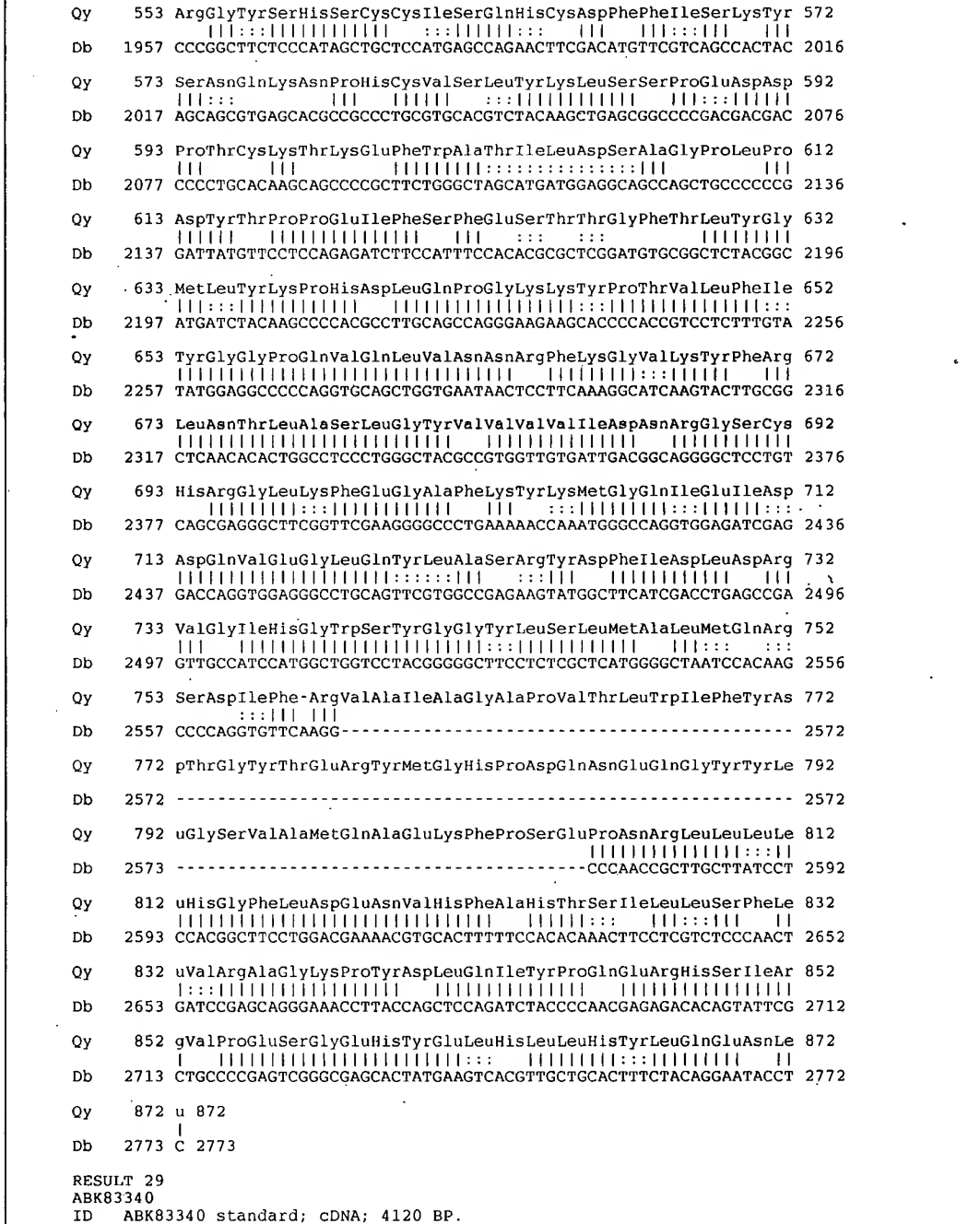

RESULT 29
ABK83340
ID ABK83340 standard; cDNA; 4120 BP.
XX

```
AC   ABK83340;
XX
DT   12-AUG-2002  (first entry)
XX
DE   cDNA encoding human DPRP-2 splice variant #8.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   P-PSDB; ABG61609.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 100-101; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ   Sequence 4120 BP; 884 A; 1298 C; 1162 G; 776 T; 0 other;

Alignment Scores:
Pred. No.:                3.98e-255      Length:          4120
Score:                    2599.50        Matches:         479
Percent Similarity:       71.82%         Conservative:    125
Best Local Similarity:    56.96%         Mismatches:      173
Query Match:              55.31%         Indels:          64
DB:                       24             Gaps:            4

US-10-070-464-1 (1-882) x ABK83340 (1-4120)

Qy      35 PheTyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuLeuAlaAspThrArgLys 54
           |||  |||:::::::::|||||     |||:::  ::::::     :::|||||
Db     436 TTCCAGGTGCAGAAGCACTCGTGGGACGGGCTCCGGAGCATCATCCACGGCAGCCGCAAG 495

Qy      55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
           |||  |||  ::::::  ||||||||||||||||||  ||||||::::::  |||
Db     496 TACTCGGGCCTCATTGTCAACAAGGCGCCCCACGACTTCCAGTTTGTGCAGAAGACGGAT 555

Qy      75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
           ||||||||||||  |||:::||||||||  |||         :::||||||
Db     556 GAGTCTGGGCCCCACTCCCACCGCCTCTACTACCTGGGAATGCCATATGGCAGCCGAGAG 615

Qy      95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
           |||:::|||  ||||||||||||||||||  :::  :::  |||:::|||:::|||
Db     616 AACTCCCTCCTCTACTCTGAGATTCCCAAGAAGGTCCGGAAAGAGGCTCTGCTGCTCCTG 675

Qy     115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
           |||||||||  :::||||||  ||||||||||||      :::|||:::||||||||
Db     676 TCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCCACCATGGGGTCTACTCTCGG 735

Qy     135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
           |||||||||||||||||||||||||||||||:::|||      ||||||  ||||||||||
Db     736 GAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACCTCCTACGAC 795

Qy     155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
           :::|||      ||||||  ||||||||||||||  :::  :::::::|||  :::
Db     796 TTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTCCACTGCCGC 855

Qy     175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
           |||||||||      ||||||      |||::::::|||      ::::::|||
Db     856 GACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATCAAGACCCAG 915

Qy     195 CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe 214
           |||         |||||||||||||:::||||||||||||||  :::  :::|||
Db     916 TGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTCTTCTCCTTC 975

Qy     215 IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArgArgLeuThr 234
           |||::::::::::|||:::|||:::::::||||||  |||  ||||||||||||||||||
Db     976 ATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGGCGGCTGACC 1035

Qy     235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
           :::  |||      |||:::|||:::  :::|||  :::||||||||||||||||||
Db    1036 TTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGTGTGGCCACC 1095

Qy     255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu 274
           ||||||:::||||||||||||||||||:::::||||||||||||||||  |||
Db    1096 TTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCCACAGCCTCC 1155

Qy     275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer 293
               |||  |||  |||  ||||||||||||||||||||  |||||||||
Db    1156 TGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTCGATGAGTCC 1215

Qy     294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
           |||||||||:::|||||||||  ||||||  ||||||  |||:::  ||||||:::
Db    1216 GAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACGGACTCGTAT 1275

Qy     314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
           |||||||||:::|||||||:::  |||||||||:::      |||:::::|||
Db    1276 CGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCTGAGTTCCAG 1335

Qy     334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
           |||:::::::|||:::|||:::         :::|||||||||:::|||||||||
Db    1336 ACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAGCCCTTCAGC 1395

Qy     354 IleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr 373
           ||||||      ||||||||||||||||||||||||||||||  :::|||||||||
Db    1396 TCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGATGGCAAATAC 1455

Qy     374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
           ||||||::::::  |||||||||  |||      ||||||:::|||||||:::  |||
Db    1456 GCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTCCTCCCCCCG 1515

Qy     394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
           ||||||||||||      ::::::      :::|||                ::::|||
Db    1516 GCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCCAGAGCTGTC 1575

Qy     414 ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle 433
           |||  :::|||  |||  ::::::|||||||||  |||::::::|||||||||:::
Db    1576 CCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGGATCAATGTT 1635

Qy     434 HisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGluPheIlePhe 452
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Db   1636 CATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGCTTTCTCCGC 1695

Qy    453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472

Db   1696 GCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTTTTAAAATCC 1755

Qy    473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492

Db   1756 CAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGGGAAGATGAATTTAAGTGCCCCATT 1815

Qy    493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHisGlySerAsn 512

Db   1816 AAGGAAGAGATTGCTCTGACCAGCGGTGAATGGGAGGTTTTGGCGAGGCACGGCTCC--- 1872

Qy    513 IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532

Db   1873 ----------------------------------AAGGGCACCAAGGACACGCCGCTG 1896

Qy    533 GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552

Db   1897 GAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGCCTCACCACG 1956

Qy    553 ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIleSerLysTyr 572

Db   1957 CCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTCAGCCACTAC 2016

Qy    573 SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAsp 592

Db   2017 AGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCCGACGACGAC 2076

Qy    593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612

Db   2077 CCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCCAGCTGCCCCCCG 2136

Qy    613 AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632

Db   2137 GATTATGTTCCTCCAGAGATCTTCCATTTCCACACGCGCTCGGATGTGCGGCTCTACGGC 2196

Qy    633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652

Db   2197 ATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTCCTCTTTGTA 2256

Qy    653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672

Db   2257 TATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAGTACTTGCGG 2316

Qy    673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692

Db   2317 CTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGGGGCTCCTGT 2376

Qy    693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712

Db   2377 CAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTGGAGATCGAG 2436

Qy    713 AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732

Db   2437 GACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGACCTGAGCCGA 2496

Qy    733 ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752

Db   2497 GTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTAATCCACAAG 2556

Qy    753 SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAs 772

Db   2557 CCCCAGGTGTTCAAGG---------------------------------------------- 2572

Qy    772 pThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrLe 792

Db   2572 ---------------------------------------------------------- 2572

Qy    792 uGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuLe 812

Db   2573 ----------------------------------------CCCAACCGCTTGCTTATCCT 2592

Qy    812 uHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe 832

Db   2593 CCACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTCTCCCAACT 2652

Qy    832 uValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleAr 852

Db   2653 GATCCGAGCAGGGAAACCTTACCAGCTCCAGATCTACCCCAACGAGAGACACAGTATTCG 2712

Qy    852 gValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLe 872

Db   2713 CTGCCCCGAGTCGGGCGAGCACTATGAAGTCACGTTGCTGCACTTTCTACAGGAATACCT 2772

Qy    872 u 872

Db   2773 C 2773
```

RESULT 30
AAI57880
ID AAI57880 standard; cDNA; 3262 BP.
XX
AC AAI57880;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 83.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM38724.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 83; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as

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CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 3262 BP; 687 A; 1019 C; 931 G; 625 T; 0 other;

Alignment Scores:
Pred. No.:                1.09e-242      Length:          3262
Score:                    2476.50        Matches:         462
Percent Similarity:       74.12%         Conservative:    125
Best Local Similarity:    58.33%         Mismatches:      166
Query Match:              52.69%         Indels:          40
DB:                       22             Gaps:            6

US-10-070-464-1 (1-882) x AAI57880 (1-3262)

Qy      92 AsnArgGluAsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaVal 111
           :::|||||||||:::|||   |||||||||||||||      :::   :::   |||:::
Db      41 AGCCGAGAGAACTCCCTCCTCTACTCTGAGATTCCATT-CAAGTCCGGAAAGAGGCTCTG 99

Qy     112 LeuMetLeuSerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMet 131
           |||:::|||||||||||||   :::|||||||   ||||||||||||      :::|||:::
Db     100 CTGCTCCTGTCCTGGAAGCAGATGCTGGATCATTTCCAGGCCACGCCCCACCATGGGGTC 159

Qy     132 TyrSerArgGluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAla 151
           ||||||||||||||||||||||||||||||||||||:::|||      ||||||
Db     160 TACTCTCGGGAGGAGGAGCTGCTGAGGGAGCGGAAACGCCTGGGGGTCTTCGGCATCACC 219

Qy     152 SerTyrAspTyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyr 171
           |||||||||:::|||      ||||||   ||||||||||||||   :::   ::::::
Db     220 TCCTACGACTTCCACAGCGAGAGTGGCCTCTTCCTCTTCCAGGCCAGCAACAGCCTCTTC 279

Qy     172 HisValLysAspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuVal 191
               :::||||||||||      ||||||      |||::::::|||      :::
Db     280 CGCTGCCGCGACGGCGGCAAGAACGGCTTCATGGTGTCCCCTATGAAACCGCTGGAAATC 339

Qy     192 GluThrSerCysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrp 211
           :::|||   |||         ||||||||||||||:::|||||||||||||||   :::
Db     340 AAGACCCAGTGCTCAGGGCCCCGGATGGACCCCAAAATCTGCCCTGCCGACCCTGCCTTC 399

Qy     212 IleAlaPheIleHisSerAsnAspIleTrpIleSerAsnIleValThrArgGluGluArg 231
              :::||||||:::::::::|||:::|||:::::::||||||   |||   |||||||||
Db     400 TTCTCCTTCATCAATAACAGCGACCTGTGGGTGGCCAACATCGAGACAGGCGAGGAGCGG 459

Qy     232 ArgLeuThrTyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGly 251
           |||||||||:::   |||      |||:::|||:::   :::|||   :::||||||||||
Db     460 CGGCTGACCTTCTGCCACCAAGGTTTATCCAATGTCCTGGATGACCCCAAGTCTGCGGGT 519

Qy     252 ValAlaThrPheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysPro 271
           ||||||||||||||:::|||||||||||||||||:::::|||||||||||||||||||||
Db     520 GTGGCCACCTTCGTCATACAGGAAGAGTTCGACCGCTTCACTGGGTACTGGTGGTGCCCC 579

Qy     272 LysAlaGluThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsn 290
              |||            |||   |||   |||   ||||||||||||||||||||
Db     580 ACAGCCTCCTGGGAAGGTTCAGAGGGCCTCAAGACGCTGCGAATCCTGTATGAGGAAGTC 639

Qy     291 AspGluSerGluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAla 310
           ||||||||||||||||||:::|||||||||   ||||||   ||||||   |||:::
Db     640 GATGAGTCCGAGGTGGAGGTCATTCACGTCCCCTCTCCTGCGCTAGAAGAAAGGAAGACG 699

Qy     311 AspSerPheArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSer 330
           ||||||:::|||||||||:::|||||||:::   |||||||||:::      |||:::::::
Db     700 GACTCGTATCGGTACCCCAGGACAGGCAGCAAGAATCCCAAGATTGCCTTGAAACTGGCT 759

Qy     331 GluIleMetIleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGln 350
           |||         |||:::::::|||:::|||:::         :::|||||||||:::|||
Db     760 GAGTTCCAGACTGACAGCCAGGGCAAGATCGTCTCGACCCAGGAGAAGGAGCTGGTGCAG 819

Qy     351 ProPheGluIleLeuPheGluGlyValGluTyrIleAlaArgAlaGlyTrpThrProGlu 370
           ||||||      ||||||      ||||||||||||||||||||||||||||||   :::
Db     820 CCCTTCAGCTCGCTGTTCCCGAAGGTGGAGTACATCGCCAGGGCCGGGTGGACCCGGGAT 879

Qy     371 GlyLysTyrAlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeu 390
           ||||||||||||||::::::   |||||||||   |||      ||||||:::||||||
Db     880 GGCAAATACGCCTGGGCCATGTTCCTGGACCGGCCCCAGCAGTGGCTCCAGCTCGTCCTC 939

Qy     391 IleSerProGluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIle 410
           :::   |||   ||||||||||||      ::::::      :::|||
Db     940 CTCCCCCCGGCCCTGTTCATCCCGAGCACAGAGAATGAGGAGCAGCGGCTAGCCTCTGCC 999

Qy     411 GluSerValProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrp 430
              :::||||||   :::|||   |||   ::::::|||||||||   |||:::::::|||
Db    1000 AGAGCTGTCCCCAGGAATGTCCAGCCGTATGTGGTGTACGAGGAGGTCACCAACGTCTGG 1059

Qy     431 IleAsnIleHisAspIlePheHisValPheProGlnSerHis---GluGluGluIleGlu 449
           ||||||:::|||||||||||||:::   ||||||||||||      |||:::|||:::
Db    1060 ATCAATGTTCATGACATCTTCTATCCCTTCCCCCAATCAGAGGGAGAGGACGAGCTCTGC 1119

Qy     450 PheIlePheAlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIle 469
           |||:::   |||:::|||||||||||||||||||   ||||||||||||:::|||::::::
Db    1120 TTTCTCCGCGCCAATGAATGCAAGACCGGCTTCTGCCATTTGTACAAAGTCACCGCCGTT 1179

Qy     470 LeuLysGluSerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLys 489
           ||||||      |||      |||      |||
Db    1180 TTAAAATCCCAGGGCTACGATTGGAGTGAGCCCTTCAGCCCCGGG---------------- 1224

Qy     490 CysProIleLysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGlyArgHis 509
                  :::   |||   :::::::|||:::      |||
Db    1225 ---------GAAGGTGAGCAGAGCCTGACGAATGCTATCTGG----------------- 1257

Qy     510 GlySerAsnIleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAsp 529
                        |||:::|||      :::||||||||||||:::||||||||||
Db    1258 --------------GTCAATGAGGAGACCAAGCTGGTGTACTTCCAGGGCACCAAGGAC 1302

Qy     530 SerProLeuGluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArg 549
           :::||||||||||||||||||||||||||||||||          ||||||:::   |||
Db    1303 ACGCCGCTGGAGCACCACCTCTACGTGGTCAGCTATGAGGCGGCCGGCGAGATCGTACGC 1362

Qy     550 LeuThrAspArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheIle 569
           ||||||      |||:::||||||||||||   :::||||||:::   |||   |||:::
Db    1363 CTCACCACGCCCGGCTTCTCCCATAGCTGCTCCATGAGCCAGAACTTCGACATGTTCGTC 1422

Qy     570 SerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerPro 589
           |||   ||||||:::         |||   ||||||   :::||||||||||||   |||
Db    1423 AGCCACTACAGCAGCGTGAGCACGCCGCCCTGCGTGCACGTCTACAAGCTGAGCGGCCCC 1482

Qy     590 GluAspAspProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGly 609
           :::|||||||||      |||          |||||||||:::::::::::::::|||
Db    1483 GACGACGACCCCCTGCACAAGCAGCCCCGCTTCTGGGCTAGCATGATGGAGGCAGCC--- 1539

Qy     610 ProLeuProAspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThr 629
                                  :::||||||   |||   :::   :::
Db    1540 ----------------------AAGATCTTCCATTTCCACACGCGCTCGGATGTGCGG 1575

Qy     630 LeuTyrGlyMetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrVal 649
           ||||||||||||:::||||||||||   ||||||||||||||||:::||||||||||
Db    1576 CTCTACGGCATGATCTACAAGCCCCACGCCTTGCAGCCAGGGAAGAAGCACCCCACCGTC 1635

Qy     650 LeuPheIleTyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLys 669
           ||||||:::||||||||||||||||||||||||||||||||   |||||||||:::|||
Db    1636 CTCTTTGTATATGGAGGCCCCCAGGTGCAGCTGGTGAATAACTCCTTCAAAGGCATCAAG 1695

Qy     670 TyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArg 689
           |||  ||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db    1696 TACTTGCGGCTCAACACACTGGCCTCCCTGGGCTACGCCGTGGTTGTGATTGACGGCAGG 1755

Qy     690 GlySerCysHisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIle 709
           |||||||||   |||||||||:::||||||||||||   |||   :::||||||||:::
Db    1756 GGCTCCTGTCAGCGAGGGCTTCGGTTCGAAGGGGCCCTGAAAAACCAAATGGGCCAGGTG 1815
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```
Qy    710 GluIleAspAspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAsp 729
          ||||||:::||||||||||||||||||||||:::::|||   :::|||  |||||||||
Db   1816 GAGATCGAGGACCAGGTGGAGGGCCTGCAGTTCGTGGCCGAGAAGTATGGCTTCATCGAC 1875

Qy    730 LeuAspArgValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeu 749
          |||  ||||||  ||||||||||||||||||||||:::|||||||||||  |||
Db   1876 CTGAGCCGAGTTGCCATCCATGGCTGGTCCTACGGGGGCTTCCTCTCGCTCATGGGGCTA 1935

Qy    750 MetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIle 769
          :::  :::     :::|||:::|||||||||||||||||||||||:::|||:::
Db   1936 ATCCACAAGCCCCAGGTGTTCAAGGTGGCCATCGCGGGTGCCCCGGTCACCGTCTGGATG 1995

Qy    770 PheTyrAspThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnGly 789
          ||||||||||||||||||||||||||||     |||:::  |||:::  |||
Db   1996 GCCTACGACACAGGGTACACTGAGCGCTACATGGACGTCCCTGAGAACAACCAGCACGGC 2055

Qy    790 TyrTyrLeuGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeu 809
          |||      ||||||||||||:::      ||||||  |||:::|||||||||||||||
Db   2056 TATGAGGCGGGTTCCGTGGCCCTGCACGTGGAGAAGCTGCCCAATGAGCCCAACCGCTTG 2115

Qy    810 LeuLeuLeuHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeu 829
          |||:::|||||||||||||||||||||||||||||||  ||||||:::  |||:::
Db   2116 CTTATCCTCCACGGCTTCCTGGACGAAAACGTGCACTTTTTCCACACAAACTTCCTCGTC 2175

Qy    830 SerPheLeuValArgAlaGlyLysProTyrAspLeu---------------------- 841
          |||  |||:::|||||||||||||||||  |||
Db   2176 TCCCAACTGATCCGAGCAGGGAAACCTTACCAGCTCCAGGTGGCCCTGCCTCCTGTCTCC 2235

Qy    842 ---GlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
             ||||||||||||  ||||||||||||||||||  ||||||||||||||||||||
Db   2236 CCGCAGATCTACCCCAACGAGAGACACAGTATTCGCTGCCCCGAGTCGGGCGAGCACTAT 2295

Qy    861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu 872
          |||:::  |||||||||:::|||||||||  |||
Db   2296 GAAGTCACGTTGCTGCACTTTCTACAGGAATACCTC 2331


Search completed: May 19, 2003, 15:54:36
Job time : 7841 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 13, 2003, 14:11:35 ; Search time 80 Seconds
(without alignments)
1469.088 Million cell updates/sec

Title: US-10-070-464-1
Perfect score: 4700
Sequence: 1 MAAAMETEQLGVEIFETADC.....HLLHYLQENLGSRIAALKVI 882

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4700	100.0	882	22	AAB47187	Human DPP8. Homo
2	4700	100.0	882	23	AAE24170	Human dipeptidyl p
3	4700	100.0	882	23	ABG61591	Human DPPIV relate
4	4700	100.0	882	23	AAU74749	Human protease PRT
5	4700	100.0	882	23	AAG78415	Amino acid sequenc
6	4118	87.6	782	23	ABB97361	Novel human protei
7	3771	80.2	724	23	ABB97362	Novel human protei
8	3504	74.6	658	23	ABG61600	Human DPRP-1 splic
9	3504	74.6	661	23	ABG61596	Human DPRP-1 splic
10	3504	74.6	690	23	ABG61594	Human DPRP-1 splic
11	3333.5	70.9	632	22	AAB93565	Human protein sequ
12	3236	68.9	613	23	ABG61601	Human DPRP-1 splic
13	2870	61.1	863	23	ABG61592	Human DPPIV relate
14	2870	61.1	892	23	ABG61602	Human DPRP-2 splic
15	2870	61.1	892	23	ABG61604	Human DPRP-2 splic
16	2863	60.9	969	23	AAE24168	Human dipeptidyl p
17	2835	60.3	830	23	AAE24171	Human dipeptidyl p
18	2833	60.3	869	23	AAE24169	Alternative versio
19	2820.5	60.0	879	23	ABG61607	Human DPRP-2 splic
20	2820.5	60.0	879	23	ABG61608	Human DPRP-2 splic
21	2713.5	57.7	847	23	AAE23875	Murine dipeptidyl
22	2547.5	54.2	580	23	AAE14337	Human protease PRT
23	2422	51.5	465	22	AAB47189	Human DPP8 318Thr-
24	2413.5	51.4	737	22	AAM38724	Human polypeptide
25	2406	51.2	832	23	ABG61605	Human DPRP-2 splic
26	2406	51.2	832	23	ABG61606	Human DPRP-2 splic
27	2356.5	50.1	819	23	ABG61609	Human DPRP-2 splic
28	2356.5	50.1	819	23	ABG61610	Human DPRP-2 splic
29	2233.5	47.5	683	22	AAM40510	Human polypeptide
30	1914.5	40.7	720	21	AAB41626	Human ORFX ORF1390
31	1836.5	39.1	360	22	AAB47190	Human DPP8 244Glu-
32	1808	38.5	358	23	ABG61597	Human DPRP-1 splic
33	1754.5	37.3	497	23	ABG64845	Human albumin fusi
34	1754.5	37.3	497	23	AAU96169	Human secreted pro
35	1750.5	37.2	497	23	ABG64844	Human albumin fusi
36	1750.5	37.2	497	23	AAU96192	Human secreted pro
37	1645.5	35.0	310	22	AAB47188	Human DPP8 524Phe-
38	1645.5	35.0	310	23	ABB08994	Human dipeptidyl p
39	1643.5	35.0	508	21	AAB42928	Human ORFX ORF2692
40	1599.5	34.0	1042	22	ABB60137	Drosophila melanog
41	1599.5	34.0	1102	22	ABB62029	Drosophila melanog
42	1400	29.8	518	21	AAY90299	Human peptidase, H
43	1391	29.6	518	23	ABG61603	Human DPRP-2 splic
44	1278	27.2	241	23	ABG61595	Human DPRP-1 splic
45	1182	25.1	460	22	AAM38740	Human polypeptide

ALIGNMENTS

RESULT 1
AAB47187
ID AAB47187 standard; Protein; 882 AA.
XX
AC AAB47187;
XX
DT 29-JUN-2001 (first entry)
XX
DE Human DPP8.
XX
KW Human; dipeptidyl aminopeptidase; DPP8; prolyl oligopeptidase;
KW dipeptidyl peptidase; DPPIV; T cell; cleavage; diarrhoea;
KW growth hormone deficiency; glucose level; mucosal regeneration;
KW non-insulin dependent diabetes mellitus;glucose intolerance;
KW immunosuppression.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Active-site 739
FT /note= "Forms part of Ser-Asp-His catalytic triad"
FT Active-site 817
FT /note= "Forms part of Ser-Asp-His catalytic triad"
FT Active-site 849
FT /note= "Forms part of Ser-Asp-His catalytic triad"
XX
PN WO200119866-A1.
XX
PD 22-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-AU01085.
XX
PR 10-SEP-1999; 99AU-0002762.

PR 18-FEB-2000; 2000AU-0005709.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorell MD;
XX
DR WPI; 2001-281520/29.
DR N-PSDB; AAC85694.
XX
PT New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
PT substrates, identifying inhibitors of DPP8 catalytic activity which
PT have therapeutic uses, and for detecting activated T cells -
XX
PS Claim 1; Fig 2; 78pp; English.
XX
CC This sequence represents human dipeptidyl aminopeptidase (DPP8).
CC DPP8 has substrate specificity for H-Ala-Pro-pNA, H-Gly-Pro-pNA and
CC H-Arg-Pro-pNA. Therefore, it is a prolyl oligopeptidase and a
CC dipeptidyl peptidase, because it is capable of hydrolysing the
CC peptide bond C-terminal to Pro in each of these compounds. DPP8
CC is homologous with human DPPIV. DPP8 is useful for cleaving a
CC substrate, and for detecting an activated T cell which involves
CC measuring the level of DPP8 gene expression in a T cell. The level
CC of DPP8 expression is detected by detecting the amount of DPP8 RNA
CC in the cell. It is also useful for identifying a molecule capable
CC of inhibiting the cleavage of the substrate by DPP8. Molecules
CC identified as inhibiting DPP8 catalytic activity may be useful for
CC treating diarrhoea, growth hormone deficiency, lowering glucose levels
CC in non-insulin dependent diabetes mellitus and other disorders
CC involving glucose intolerance, enhancing mucosal regeneration and
CC as immunosuppressants.
XX
SQ Sequence 882 AA;

Query Match 100.0%; Score 4700; DB 22; Length 882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||||||||||||||||||||||
Db    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
```

RESULT 2
AAE24170
ID AAE24170 standard; Protein; 882 AA.
XX
AC AAE24170;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human dipeptidyl peptidase 8 (DPP8) protein.
XX
KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme.
XX
OS Homo sapiens.
XX
PN WO200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-AU01388.
XX
PR 27-OCT-2000; 2000AU-0001078.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD;
XX
DR WPI; 2002-454646/48.
DR N-PSDB; AAD38956.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Example; Fig 1; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is human DPP8 protein.
XX
SQ Sequence 882 AA;

```
  Query Match           100.0%;  Score 4700;  DB 23;  Length 882;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  882;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
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Db     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
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Db     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy     601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660

Qy     661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Qy     721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780

Qy     781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840

Qy     841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
           |||||||||||||||||||||||||||||||||||||||||||
Db     841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882


RESULT 3
ABG61591
ID   ABG61591 standard; Protein; 882 AA.
XX
AC   ABG61591;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human DPPIV related serine protease DPRP-1.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83322.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Claim 17; Fig 1; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   882 AA;

  Query Match           100.0%;  Score 4700;  DB 23;  Length 882;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  882;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
```

```
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
Db    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
Db    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
Db    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
Db    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
```

RESULT 4
AAU74749
ID AAU74749 standard; Protein; 882 AA.
XX
AC AAU74749;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PRTS-9 protein sequence.
XX
KW Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis.
XX
OS Homo sapiens.
XX
PN WO200198468-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US19178.
XX
PR 16-JUN-2000; 2000US-212336P.
PR 22-JUN-2000; 2000US-213955P.
PR 29-JUN-2000; 2000US-215396P.
PR 07-JUL-2000; 2000US-216821P.
PR 14-JUL-2000; 2000US-218946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM;
PI Delegeane AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA;
PI Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT;
PI Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;
PI Kallick DA;
XX
DR WPI; 2002-090437/12.
DR N-PSDB; ABK12892.
XX
PT Twenty one human proteases (referred to as PRTS-1 to PRTS-21), useful
PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
PT proliferative (e.g. cancer)disorders -
XX
PS Claim 1; Page 140-142; 177pp; English.
XX
CC The present invention relates to twenty one new human proteases,
CC referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
CC myocardial infarction, autoimmune/inflammatory e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
CC endometriosis disorders. Numerous other examples of each disorder are
CC given in the specification. The present protein sequence represents
CC the human protease PRTS-9 protein of the invention.
XX
SQ Sequence 882 AA;

Query Match 100.0%; Score 4700; DB 23; Length 882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
Db    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
Db    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
```

```
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||||||||||||||||||||||
Db    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
```

```
RESULT 5
AAG78415
ID   AAG78415 standard; Protein; 882 AA.
XX
AC   AAG78415;
XX
DT   12-APR-2002  (first entry)
XX
DE   Amino acid sequence of 21953 human prolyl oligopeptidase.
XX
KW   21953 prolyl oligopeptidase; antibody; proline; endopeptidase;
KW   cancer; cardiovascular disease; autoimmune disease; atopic allergy;
KW   neuronal disorder; vascular disorder; prostate disorder; cytostatic;
KW   antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
KW   diabetes mellitus; arthritis; multiple sclerosis; asthma;
KW   Grave's disease; neuronal disorder; demyelinating disease.
XX
OS   Homo sapiens.
XX
PN   WO200179473-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US40483.
XX
PR   18-APR-2000; 2000US-197508P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers RA,  Williamson M;
XX
DR   WPI; 2002-034353/04.
DR   N-PSDB; AAH99934.
XX
PT   New polypeptides 21953, member of human prolyl oligopeptidase family,
PT   useful as diagnostic targets and therapeutic agents for controlling
PT   cancer, lymphoma and leukemia  -
XX
PS   Claim 1; Page 102-103; 121pp; English.
XX
CC   This invention relates to an isolated 21953 human prolyl
CC   oligopeptidase. Which is cytostatic, antidiabetic, antiarthritic,
CC   neuroprotective, antithyroid, dermatological, antipsoriatic,
CC   antiasthmatic, ophthalmological, antiinflammatory, nootropic,
CC   antiparkinsonian, anticonvulsant, gynaecological, vasotropic,
CC   antianginal, cardiant, antiatherosclerotic, anorectic and
CC   metabolic in its action. Uses include gene therapy, expression or
CC   activity of 21953 protein modulator, it is useful for identifying a
CC   compound which binds to it and can be used in preventing, treating
CC   or detecting a cellular proliferative or differentiative disorder.
CC   The 21953 molecules can act as novel diagnostic targets and therapeutic
CC   agents for controlling disorders associated with the aberrant activity
CC   or degradation of peptide hormones e.g., disorders associated with cell
CC   differentiation and proliferation such as cancer, immune function,
CC   reproductive, neurological and cardiovascular function. The 21953
CC   molecules are thus useful for treating and preventing cellular
CC   proliferative and differentiative disorders, haematopoietic neoplastic
CC   disorders, immune disorders such as autoimmune diseases, diabetes
CC   mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
CC   neuronal disorders, demyelinating diseases, vascular disorders and
CC   metabolism or pain disorders. This sequence represents the amino
CC   acid sequence of 21953 human prolyl oligopeptidase.
XX
SQ   Sequence   882 AA;
```

```
  Query Match             100.0%;  Score 4700;  DB 23;  Length 882;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  882;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||||||||||||||||||||||
Db    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882


RESULT 6
ABB97361
ID   ABB97361 standard; Protein; 782 AA.
XX
AC   ABB97361;
XX
DT   27-JUN-2002  (first entry)
XX
DE   Novel human protein SEQ ID NO: 629.
XX
KW   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW   antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW   neuroprotective; antiparkinsonian; protein therapy; EST;
KW   expressed sequence tag.
XX
OS   Homo sapiens.
XX
PN   WO200222660-A2.
XX
PD   21-MAR-2002.
XX
PF   10-SEP-2001; 2001WO-US26015.
XX
PR   11-SEP-2000; 2000US-0659671.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Wehrman T,  Drmanac RT;
XX
DR   WPI; 2002-292408/33.
DR   N-PSDB; ABN32547.
XX
PT   An isolated polynucleotide for treating diseases associated with its
PT   encoded polypeptide such as cancer and multiple sclerosis -
XX
PS   Example 2; SEQ ID NO 629; 509pp; English.
XX
CC   The present invention provides the protein and coding sequences of 444
CC   novel human proteins. These were isolated from expressed sequences tags
CC   (ESTs). They can be used to stimulate cell growth, to regulate
CC   haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC   e.g. in burn treatment, to regulate the immune system e.g. to treat
CC   multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC   infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC   stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC   e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC   Parkinson's disease. The present sequence is a protein of the invention.
XX
SQ   Sequence   782 AA;

  Query Match             87.6%;  Score 4118;  DB 23;  Length 782;
  Best Local Similarity   88.7%;  Pred. No. 0;
  Matches  782;  Conservative    0;  Mismatches    0;  Indels  100;  Gaps    1;

Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQ--- 657

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720

Db    658 ------------------------------------------------------------ 657

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
                                                 ||||||||||||||||||||
Db    658 -----------------------------------VAIAGAPVTLWIFYDTGYTERYM 680

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 740

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||||||||||||||||||||||
Db    741 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 782


RESULT 7
ABB97362
ID   ABB97362 standard; Protein; 724 AA.
XX
AC   ABB97362;
XX
DT   27-JUN-2002  (first entry)
XX
DE   Novel human protein SEQ ID NO: 630.
XX
KW   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW   antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW   neuroprotective; antiparkinsonian; protein therapy; EST;
KW   expressed sequence tag.
XX
OS   Homo sapiens.
XX
PN   WO200222660-A2.
```

XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR N-PSDB; ABN32548.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Example 2; SEQ ID NO 630; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.
XX
SQ Sequence 724 AA;

Query Match 80.2%; Score 3771; DB 23; Length 724;
Best Local Similarity 82.1%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 158; Gaps 2;

```
Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
          ||||
Db    121 DLFQ---------------------------------------------------------- 124

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 --QQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 182

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 242

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 302

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 362

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 422

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 482

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 542

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQ--- 599

Qy    661 VNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 ---------------------------------------------------------- 599

Qy    721 LASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM 780
                                                  ||||||||||||||||||||
Db    600 -----------------------------------VAIAGAPVTLWIFYDTGYTERYM 622

Qy    781 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    623 GHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYD 682

Qy    841 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||||||||||||||||||||||
Db    683 LQIYPQERHSIRVPESGEHYELHLLHYLQENLGSRIAALKVI 724
```

RESULT 8
ABG61600
ID ABG61600 standard; Protein; 658 AA.
XX
AC ABG61600;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human DPRP-1 splice variant #7.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;.
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR N-PSDB; ABK83331.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 70-72; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),

```
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   658 AA;

  Query Match            74.6%;  Score 3504;  DB 23;  Length 658;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  655;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy     601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655


RESULT 9
ABG61596
ID   ABG61596 standard; Protein; 661 AA.
XX
AC   ABG61596;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human DPRP-1 splice variant #3.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83327.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 63-65; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   661 AA;

  Query Match            74.6%;  Score 3504;  DB 23;  Length 661;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  655;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
```

```
Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655
```

RESULT 10
ABG61594
ID ABG61594 standard; Protein; 690 AA.
XX
AC ABG61594;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human DPRP-1 splice variant #1.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR N-PSDB; ABK83325.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 59-61; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ Sequence 690 AA;

```
  Query Match             74.6%;  Score 3504;  DB 23;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  655;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 WATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGG 655
```

RESULT 11
AAB93565
ID AAB93565 standard; Protein; 632 AA.
XX
AC AAB93565;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:12964.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX

PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 12964; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 632 AA;

Query Match 70.9%; Score 3333.5; DB 22; Length 632;
Best Local Similarity 92.4%; Pred. No. 2.3e-312;
Matches 631; Conservative 0; Mismatches 1; Indels 51; Gaps 1;

```
Qy    200 MDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQE 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQE 60

Qy    260 EFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTG 319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTG 120

Qy    320 TANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILL 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILL 180

Qy    380 DRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHV 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHV 240

Qy    440 FPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAIT 499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAIT 300

Qy    500 SGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSC 559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    301 SGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRSYSHSC 360

Qy    560 CISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEI 619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEI 420

Qy    620 FSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASL 679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 FSFESTTGFTLYGMLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASL 480

Qy    680 GYVVVVIDNRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWS 739
          ||||||||||||||||||||||||
Db    481 GYVVVVIDNRGSCHRGLKFEGAFKYKM---------------------------------- 507

Qy    740 YGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQA 799
                              ||||||||||||||||||||||||||||||||||||||||
Db    508 ------------------VAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQA 549

Qy    800 EKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEH 859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 EKFPSEPNRLLLLHGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEH 609

Qy    860 YELHLLHYLQENLGSRIAALKVI 882
          |||||||||||||||||||||||
Db    610 YELHLLHYLQENLGSRIAALKVI 632
```

RESULT 12
ABG61601
ID ABG61601 standard; Protein; 613 AA.
XX
AC ABG61601;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human DPRP-1 splice variant #8.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR N-PSDB; ABK83332.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 73-75; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related

```
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   613 AA;

  Query Match             68.9%;  Score 3236;  DB 23;  Length 613;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-303;
  Matches  607;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAAMETEQLGVEIFETADCEENIESQDRPKLEPFYVERYSWSQLKKLLADTRKYHGYMM 60

Qy      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSWKPLL 120

Qy     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLFQAGSGIYHVKDGGPQG 180

Qy     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISNIVTREERRLTYVHNEL 240

Qy     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGGKILRILYEENDESEVEIIHV 300

Qy     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDVIDKELIQPFEILFEGVE 360

Qy     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 YIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDVMERQRLIESVPDSVTPL 420

Qy     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 IIYEETTDIWINIHDIFHVFPQSHEEEIEFIFASECKTGFRHLYKITSILKESKYKRSSG 480

Qy     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLVYFEGTKDSPLEHHLYVVS 540

Qy     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVSLYKLSSPEDDPTCKTKEF 600

Qy     601 WATILDS 607
           |||||||
Db     601 WATILDS 607


RESULT 13
ABG61592
ID   ABG61592 standard; Protein; 863 AA.
XX
AC   ABG61592;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human DPPIV related serine protease DPRP-2.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83323.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Claim 17; Fig 1; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   863 AA;

  Query Match             61.1%;  Score 2870;  DB 23;  Length 863;
  Best Local Similarity   61.5%;  Pred. No. 2.3e-267;
  Matches  517;  Conservative  134;  Mismatches  187;  Indels    2;  Gaps    2;

Qy      35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
           | |:::||  |: ::  :||| | :: |||||| ||:: |  |||| |:||| |   :||
Db      24 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYCSRE 83

Qy      95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
           |:| |||||| : : |:|:|||| :|| |||  :|:|||||||||||||:|  || |||
Db      84 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 143

Qy     155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
           :|  || ||||| : ::| :|||  ||   |::|  ::| |   |||||:||||| : :|
Db     144 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 203

Qy     215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
           |:::|:|::|| | |||||: |  |:|: :| :|||||||:||||||::|||||| |
Db     204 INNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 263

Qy     275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
             | | |||||||| ||||||:||| || || |: ||:|||:||: |||:  |::|
Db     264 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 323
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Qy    334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
Db    324 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 383

Qy    394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452
Db    384 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 443

Qy    453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512
Db    444 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGSK 503

Qy    513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572
Db    504 IWVNEETKLVYFQGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 563

Qy    573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632
Db    564 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 623

Qy    633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692
Db    624 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 683

Qy    693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752
Db    684 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 743

Qy    753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812
Db    744 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 803

Qy    813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
Db    804 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 863
```

RESULT 14
ABG61602
ID ABG61602 standard; Protein; 892 AA.
XX
AC ABG61602;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human DPRP-2 splice variant #1.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX
DR WPI; 2002-444178/47.
DR N-PSDB; ABK83333.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT -
XX
PS Disclosure; Page 76-78; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ Sequence 892 AA;

Query Match 61.1%; Score 2870; DB 23; Length 892;
Best Local Similarity 61.5%; Pred. No. 2.4e-267;
Matches 517; Conservative 134; Mismatches 187; Indels 2; Gaps 2;

```
Qy     35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
Db     53 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRE 112

Qy     95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
Db    113 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 172

Qy    155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
Db    173 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 232

Qy    215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
Db    233 INNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 292

Qy    275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
Db    293 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 352

Qy    334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
Db    353 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 412

Qy    394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452
Db    413 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 472

Qy    453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512
Db    473 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGSK 532

Qy    513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572
Db    533 IWVNEETKLVYFQGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 592

Qy    573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632
Db    593 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 652

Qy    633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692
Db    653 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 712

Qy    693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752
```

```
          |||:|||| | :|||:||:|||||||::| :| |||| || ||||||||:|||| |: :
Db    713 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 772

Qy    753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812
          :|:|||||||||:|: |||||||||  |: |: ||  ||||:  || |:||||||:|
Db    773 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 832

Qy    813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
          |||||||||| ||: |:| |:|||||| ||||| |||||| ||||||||: |||:||| |
Db    833 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 892


RESULT 15
ABG61604
ID   ABG61604 standard; Protein; 892 AA.
XX
AC   ABG61604;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human DPRP-2 splice variant #3.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83335.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   .
XX
PS   Disclosure; Page 81-84; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   892 AA;

  Query Match             61.1%;  Score 2870;  DB 23;  Length 892;
  Best Local Similarity   61.5%;  Pred. No. 2.4e-267;
  Matches  517;  Conservative  134;  Mismatches  187;  Indels    2;  Gaps    2;

Qy      35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
           | |:::|| |: ::  :||| | :: |||||| ||:: |  |||| |:||| |   :||
Db      53 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRE 112

Qy      95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
           |:| |||||| : : |:|:|||| :|| |||  :|:|||||||||||||:|  || |||
Db     113 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 172

Qy     155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
           :|  || ||||| : ::| :|||  ||   |::|  ::| |   |||||:||||| : :|
Db     173 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 232

Qy     215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
           |:::|:|::|| | ||||||: |  |:|: :| :|||||||:||||||::|||||| |
Db     233 INNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 292

Qy     275 TTPSGGKILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
             | | | ||||||| ||||||:||| || || |: ||:|||:||: |||:  |::|
Db     293 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 352

Qy     334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
           |::|:|:   :|||:|||  ||  |||||||||| :||||:: ||| |  ||:||: |
Db     353 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 412

Qy     394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452
           ||||  ::  :|     :|| :| | ::||| |::|||:|||: ||||  |:|: |:
Db     413 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 472

Qy     453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512
           |:|||||| ||||:|::||   |  |   |   :||||||||||:|||||||| ||||
Db     473 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGSK 532

Qy     513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572
           | |:|  :||||:||||:||||||||||   ||: |||  |:|||| :||: | |:| |
Db     533 IWVNEETKLVYFQGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 592

Qy     573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632
           |:   | || :|||| |:||| |   |||:::::|   ||| ||||| | : :   |||
Db     593 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 652

Qy     633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692
           |:|||| |||||:|||||:|||||||||| |||:|| |||||||||| |||| ||||
Db     653 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 712

Qy     693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752
           |||:|||| | :|||:||:|||||||::| :| |||| || ||||||||:|||| |: :
Db     713 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 772

Qy     753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812
           :|:|||||||||:|: |||||||||  |: |: ||  ||||:  || |:||||||:|
Db     773 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 832

Qy     813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
           |||||||||| ||: |:| |:|||||| ||||| |||||||||: |||:||| |
Db     833 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 892


RESULT 16
AAE24168
ID   AAE24168 standard; Protein; 969 AA.
XX
AC   AAE24168;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human dipeptidyl peptidase 9 (DPP9) protein.
XX
KW   Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW   autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW   graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 374
FT                   /note= "Encoded by GAA"
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
DR   WPI; 2002-454646/48.
DR   N-PSDB; AAD38954.
XX
PT   New dipeptidyl peptidase (DPP) peptides, useful for screening
PT   inhibitors of DPP catalytic activity, which may be employed to treat
PT   e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT   rejection and HIV infection -
XX
PS   Claim 1; Fig 4; 91pp; English.
XX
CC   The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC   polynucleotides encoding such proteins. The DPP peptides are useful for
CC   screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC   for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC   rejection and HIV (human immuno deficiency virus) infection. The present
CC   sequence is human DPP9 protein.
XX
SQ   Sequence   969 AA;

  Query Match             60.9%;  Score 2863;  DB 23;  Length 969;
  Best Local Similarity   61.4%;  Pred. No. 1.3e-266;
  Matches  516;  Conservative  134;  Mismatches  188;  Indels    2;  Gaps    2;

Qy      35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
           | |:::|| |: ::  :||| | :: |||||| ||:: |  |||| |:||| |   :||
Db     130 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRE 189

Qy      95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
           |:| |||||| : : |:|:|||| :|| |||| :|:|||||||||||||:|  ||.|||
Db     190 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 249

Qy     155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
           :|  || ||||| : ::| :||| ||   |::|  ::| |   |||||:||||| : .:|
Db     250 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 309

Qy     215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
           :::|:|::|| | |||||: |  |:|: :| :||||||||:||||||::|||||| |
Db     310 NNNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 369

Qy     275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
             | | | ||||||| ||||||:||| || || |: ||:|||:||: |||:  |::|
Db     370 WEGSQGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 429

Qy     334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
           |::|:|:   :|||:|||  ||. |||||||||| :|||||:: ||| |  ||:||: |
Db     430 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 489

Qy     394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452
           ||||  ::  :|    :|| :| | ::||| |::|||:||||: ||||  |:|: |:
Db     490 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 549

Qy     453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512
           |:|||||| ||||:|::||   |  |    |   :||||||||||:|||||||| ||||
Db     550 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGSK 609

Qy     513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572
           | |:.|  :||||:||||:||||||||||    ||: |||  |:|||| :||: | |:| |
Db     610 IWVNEETKLVYFQGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 669

Qy     573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632
           |:   | || :|||| |:||| |   |||::::|   ||| ||||| | : :   |||
Db     670 SSVSTPPCVHVYKLSGPDDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 729

Qy     633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692
           |:|||| ||||||:|||||:|||||||||| |||:|| |||||||||| ||||| ||||
Db     730 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 789

Qy     693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752
            |||:|||| | :|||:||:|||||||::| :| |||| || ||||||||:|||| |: :
Db     790 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 849

Qy     753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812
           .:|:|||||||||:|: ||||||||||  |: |: ||  ||||:  || |:|||||:|
Db     850 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 909

Qy     813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
           |||||||||| ||: |:| |:|||||| ||||| |||||| ||||||||: |||:||| |
Db     910 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 969


RESULT 17
AAE24171
ID   AAE24171 standard; Protein; 830 AA.
XX
AC   AAE24171;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Human dipeptidyl peptidase 4 (DPP4)-like 2 protein.
XX
KW   Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW   autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW   graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme; DPP-4 like 2 protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 235
FT                   /note= "Encoded by GAG"
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
DR   WPI; 2002-454646/48.
DR   N-PSDB; AAD38957.
XX
PT   New dipeptidyl peptidase (DPP) peptides, useful for screening
PT   inhibitors of DPP catalytic activity, which may be employed to treat
PT   e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT   rejection and HIV infection -
XX
PS   Disclosure; Page 82-86; 91pp; English.
XX
CC   The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC   polynucleotides encoding such proteins. The DPP peptides are useful for
CC   screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC   for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
```

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CC   rejection and HIV (human immuno deficiency virus) infection. The present
CC   sequence is human DPP4-like 2 protein.
XX
SQ   Sequence   830 AA;

  Query Match           60.3%;  Score 2835;  DB 23;  Length 830;
  Best Local Similarity  61.7%;  Pred. No. 5.2e-264;
  Matches  512;  Conservative  131;  Mismatches  185;  Indels    2;  Gaps    2;

Qy      45 LKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRENTLFYSEIPK 104
           |: ::  :||| | :: |||||| ||:: |  |||| |:||| |   :|||:| ||||||
Db       1 LRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPK 60

Qy     105 TINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYDYHQGSGTFLF 164
           : : |:|:|||| :|| |||| :|:|||||||||||||:|  || |||:|  || |||
Db      61 KVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYDFHSESGLFLF 120

Qy     165 QAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSNDIWISN 224
           || : ::| :||| ||  |::|  ::| |  |||||:|||||: :| ::::|:|::|
Db     121 QASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFNNNSDLWVAN 180

Qy     225 IVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAETTPSGG-KIL 283
           | | |||||: |  |:|: :| :|||||||:||||||::|||||| |    | | | |
Db     181 IETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASWEGSQGLKTL 240

Qy     284 RILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIMIDAEGRIIDV 343
           |||||| ||||||:||| || || |: ||:|||:||: |||:  |::|   |::|:|:
Db     241 RILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVST 300

Qy     344 IDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISPELFIPVEDDV 403
           :|||:|||  ||  |||||||||| :|||||:: ||| |  ||:||: | ||||  ::
Db     301 QEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENE 360

Qy     404 MERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIFASECKTGFRH 462
           :|     :|| :| | ::||| |::|||:||||: ||||  |:|: |: |:|||||| |
Db     361 EQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLRANECKTGFCH 420

Qy     463 LYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSNIQVDEVRRLV 522
           |||:|::||   |  |    |   :|||||||||:|||||||| |||| | |:|  :||
Db     421 LYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGSKIWVNEETKLV 480

Qy     523 YFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKYSNQKNPHCVS 582
           ||:||||:|||||||||   ||: |||  |:|||| :||: | |:| ||:   | ||
Db     481 YFQGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVH 540

Qy     583 LYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYGMLYKPHDLQP 642
           :|||| |:||  |   |||:::::|   ||| ||||| | : :   ||||:|||| |||
Db     541 VYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYGMIYKPHALQP 600

Qy     643 GKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSCHRGLKFEGAF 702
           |||:|||||:|||||||||| |||:|| |||||||||| ||||| |||| |||:||||
Db     601 GKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSCQRGLRFEGAL 660

Qy     703 KYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQRSDIFRVAIAG 762
           | :|||:||:||||||||:| :| |||| || |||||||:|||| |: :  :|:|||||
Db     661 KNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAG 720

Qy     763 APVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLLHGFLDENVHF 822
           ||||:|: |||||||||| |: |: ||  |||:  || |:|||||:|||||||||||
Db     721 APVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILHGFLDENVHF 780

Qy     823 AHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
           ||: |:| |:|||||| ||||| |||||| ||||||||: |||:||| |
Db     781 FHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 830


RESULT 18
AAE24169
ID   AAE24169 standard; Protein; 869 AA.
XX
AC   AAE24169;
XX
DT   23-SEP-2002 (first entry)

XX
DE   Alternative version of murine dipeptidyl peptidase 9 (DPP9) protein.
XX
KW   Murine; dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;
KW   human immuno deficiency virus; graft rejection; cytostatic; autoimmunity;
KW   type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;
KW   antiviral; enzyme.
XX
OS   Mus sp.
XX
PN   WO200234900-A1.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-AU01388.
XX
PR   27-OCT-2000; 2000AU-0001078.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Abbott CA,  Gorrell MD;
XX
DR   WPI; 2002-454646/48.
DR   N-PSDB; AAD38955.
XX
PT   New dipeptidyl peptidase (DPP) peptides, useful for screening
PT   inhibitors of DPP catalytic activity, which may be employed to treat
PT   e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT   rejection and HIV infection -
XX
PS   Claim 1; Page 70-74; 91pp; English.
XX
CC   The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC   polynucleotides encoding such proteins. The DPP peptides are useful for
CC   screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC   for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC   rejection and HIV (human immuno deficiency virus) infection. The present
CC   sequence is an alternative version of murine DPP9 protein.
CC   Note: This sequence is stated to be the same as that shown as
CC   SEQ ID NO: 4 in the sequence listing of the specification. However these
CC   sequences differ.
XX
SQ   Sequence   869 AA;

  Query Match           60.3%;  Score 2833;  DB 23;  Length 869;
  Best Local Similarity  60.8%;  Pred. No. 8.7e-264;
  Matches  511;  Conservative  134;  Mismatches  193;  Indels    2;  Gaps    2;

Qy      35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
           | |:::||  |: ::  :||  | :::|||||| ||:: |  |||| |:||| |   :||
Db      30 FCVQKHSWDGLRSIIHGSRKSSGLIVSKAPHDFQFVQKPDESGPHSHRLYYLGMPYGSRE 89

Qy      95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
           |:| |||||| : : |:|:|||| :|| |||| :|:|||||||||||||:|  || |||
Db      90 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 149

Qy     155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
           :|  || ||||| : ::| :|||  ||   |::|  ::| |  |||||:||||| : :|
Db     150 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 209

Qy     215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
           |:::|:|::|| | |||||: |   | : :: :|||||||:||||||::| |||| |
Db     210 INNSDLWVANIETGEERRLTFCHQGSAGVLDNPKSAGVATFVIQEEFDRFTGCWWCPTAS 269

Qy     275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
             | | |||||| ||||||:||| || || |: ||:|||:||: |||:  |::|:
Db     270 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAELQ 329

Qy     334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
           | :|:|:   :|||:|||  ||  |||||||||| :|||||:: ||| | |||:||: |
Db     330 TDHQGKIVSSCEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQRLQLVLLPP 389

Qy     394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452
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Db    390 ALFIPAVESEAQRQAAARAVPKNVQPFVIYEEVTNVWINVHDIFHPFPQAEGQQDFCFLR 449

Qy    453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512

Db    450 ANECKTGFCHLYRVTVELKTKDYDWTEPLSPTEGEFKCPIKEEVALTSGEWEVLSRHGSK 509

Qy    513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572

Db    510 IWVNEQTKLVYFQGTKDTPLEHHLYVVSYESAGEIVRLTTLGFSHSCSMSQSFDMFVSHY 569

Qy    573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632

Db    570 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAANCPPDYVPPEIFHFHTRADVQLYG 629

Qy    633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692

Db    630 MIYKPHTLQPGRKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 689

Qy    693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752

Db    690 QRGLHFEGALKNQMGQVEIEDQVEGLQYVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 749

Qy    753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812

Db    750 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQQGYEAGSVALHVEKLPNEPNRLLIL 809

Qy    813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872

Db    810 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCRESGEHYEVTLLHFLQEHL 869


RESULT 19
ABG61607
ID   ABG61607 standard; Protein; 879 AA.
XX
AC   ABG61607;
XX
DT   12-AUG-2002 (first entry)
XX
DE   Human DPRP-2 splice variant #6.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83338.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 91-93; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   879 AA;

  Query Match             60.0%;  Score 2820.5;  DB 23;  Length 879;
  Best Local Similarity   60.7%;  Pred. No. 1.4e-262;
  Matches  510;  Conservative  132;  Mismatches  183;  Indels   15;  Gaps    3;

Qy     35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94

Db     53 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRE 112

Qy     95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154

Db    113 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 172

Qy    155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214

Db    173 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 232

Qy    215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274

Db    233 INNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 292

Qy    275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333

Db    293 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 352

Qy    334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393

Db    353 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 412

Qy    394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWINIHDIFHVFPQSH-EEEIEFIF 452

Db    413 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 472

Qy    453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512

Db    473 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGS- 531

Qy    513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572

Db    532 -----------KGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 579

Qy    573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632

Db    580 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 639

Qy    633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692

Db    640 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 699

Qy    693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752

Db    700 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 759

Qy    753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812

Db    760 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 819
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Qy    813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
          ||||||||||| ||: |:| |:|||||| ||||| |||||| |||||||: |||:||| |
Db    820 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 879


RESULT 20
ABG61608
ID   ABG61608 standard; Protein; 879 AA.
XX
AC   ABG61608;
XX
DT   12-AUG-2002 (first entry)
XX
DE   Human DPRP-2 splice variant #7.
XX
KW   Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200231134-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US31874.
XX
PR   12-OCT-2000; 2000US-240117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Qi S,  Akinsanya KO,  Riviere PJ,  Junien J;
XX
DR   WPI; 2002-444178/47.
DR   N-PSDB; ABK83339.
XX
PT   New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Disclosure; Page 95-96; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, or
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory and
CC   metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ   Sequence   879 AA;

  Query Match             60.0%;  Score 2820.5;  DB 23;  Length 879;
  Best Local Similarity   60.7%;  Pred. No. 1.4e-262;
  Matches  510;  Conservative  132;  Mismatches  183;  Indels   15;  Gaps    3;

Qy     35 FYVERYSWSQLKKLLADTRKYHGYMMAKAPHDFMFVKRNDPDGPHSDRIYYLAMSGENRE 94
          | |:::|| |: ::  :||| | :: |||||| ||:: |  |||| |:||| |   :||
Db     53 FQVQKHSWDGLRSIIHGSRKYSGLIVNKAPHDFQFVQKTDESGPHSHRLYYLGMPYGSRE 112

Qy     95 NTLFYSEIPKTINRAAVLMLSWKPLLDLFQATLDYGMYSREEELLRERKRIGTVGIASYD 154
          |:| |||||| : : |:|:|||| :|| |||| :|:|||||||||||||:|  || |||
Db    113 NSLLYSEIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYD 172

Qy    155 YHQGSGTFLFQAGSGIYHVKDGGPQGFTQQPLRPNLVETSCPNIRMDPKLCPADPDWIAF 214
          . :|  || ||||| : ::| :||| ||   |::|  ::| |  |||||:||||| : :|
Db    173 FHSESGLFLFQASNSLFHCRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSF 232

Qy    215 IHSNDIWISNIVTREERRLTYVHNELANMEEDARSAGVATFVLQEEFDRYSGYWWCPKAE 274
          |:::|:|::|| | |||||: |  |:|: :| :|||||||:|||||||::|||||| |
Db    233 INNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTAS 292

Qy    275 TTPSGG-KILRILYEENDESEVEIIHVTSPMLETRRADSFRYPKTGTANPKVTFKMSEIM 333
             | | |||||||| ||||||:||| || || |: ||:|||:||: |||:  |::|
Db    293 WEGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIALKLAEFQ 352

Qy    334 IDAEGRIIDVIDKELIQPFEILFEGVEYIARAGWTPEGKYAWSILLDRSQTRLQIVLISP 393
          |::|:|:   :|||:||| ||  |||||||||| :|||||:: ||| |  ||:||: |
Db    353 TDSQGKIVSTQEKELVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLLPP 412

Qy    394 ELFIPVEDDVMERQRLIESVPDSVTPLIIYEETTDIWININHDIFHVFPQSH-EEEIEFIF 452
          ||||  ::  :|     :|| :| | ::||| |::|||:|||||: ||||  |:|: |:
Db    413 ALFIPSTENEEQRLASARAVPRNVQPYVVYEEVTNVWINVHDIFYPFPQSEGEDELCFLR 472

Qy    453 ASECKTGFRHLYKITSILKESKYKRSSGGLPAPSDFKCPIKEEIAITSGEWEVLGRHGSN 512
          |:|||||| ||||:|::||   | |    |   :||||||||||:|||||||| ||||
Db    473 ANECKTGFCHLYKVTAVLKSQGYDWSEPFSPGEDEFKCPIKEEIALTSGEWEVLARHGS- 531

Qy    513 IQVDEVRRLVYFEGTKDSPLEHHLYVVSYVNPGEVTRLTDRGYSHSCCISQHCDFFISKY 572
                  :||||:|||||||||||   ||: |||  |:|||| :||: | |:| |
Db    532 -----------KGTKDTPLEHHLYVVSYEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHY 579

Qy    573 SNQKNPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYG 632
          |:   | || :|||| |:||| |   |||:::::|   ||| ||||| | : :   |||
Db    580 SSVSTPPCVHVYKLSGPDDDPLHKQPRFWASMMEAASCPPDYVPPEIFHFHTRSDVRLYG 639

Qy    633 MLYKPHDLQPGKKYPTVLFIYGGPQVQLVNNRFKGVKYFRLNTLASLGYVVVVIDNRGSC 692
          |:|||| ||||||:|||||:|||||||||| |||:|| |||||||||| ||||| ||||
Db    640 MIYKPHALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGYAVVVIDGRGSC 699

Qy    693 HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMQR 752
          |||:|||| | :|||:||:|||||||::| :| |||| || |||||||:|||| |: :
Db    700 QRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKYGFIDLSRVAIHGWSYGGFLSLMGLIHK 759

Qy    753 SDIFRVAIAGAPVTLWIFYDTGYTERYMGHPDQNEQGYYLGSVAMQAEKFPSEPNRLLLL 812
            :|:|||||||||:|: |||||||||| |: |: ||  ||||:  || |:|||||:|
Db    760 PQVFKVAIAGAPVTVWMAYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLIL 819

Qy    813 HGFLDENVHFAHTSILLSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENL 872
          |||||||||| ||: |:| |:|||||| ||||| |||||| |||||||: |||:||| |
Db    820 HGFLDENVHFFHTNFLVSQLIRAGKPYQLQIYPNERHSIRCPESGEHYEVTLLHFLQEYL 879


Search completed: May 13, 2003, 14:20:39
Job time : 86 secs
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